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(without alignments) 5104.524 Million cell updates/sec
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003. Compugen Ltd.
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ALIGNMENTS

RESULT 1 AAY56803 IID AAY56803 standard; Protein; 415 AA. XX

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This represents a human protein C polypeptide having a light chain and a truncated heavy chain. The protein can be produced by standard recombinant methodologies. The truncated protein C is used to treat a wide range of thrombotic or vascular disorders or hypercoagulable states, e.g. stroke; myocardial infarction; unstable anglina; sepsis; adult respiratory distress syndrome; sickle cell anemia etc. The truncated protein C retains the activity of full-length protein C but does not undergo C-terminal cleavage, of the heavy chain, during activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polypeptide useful for treating thrombotic and vascular diseases
                                                                                 Protein C; truncated; thrombotic disorder; vascular disorder; stroke; hypercoaqulable state; myocardial infarction; unstable angina; sepsis; adult respiratory distress syndrome; sickle cell anemia; human.
                                                            Truncated human protein C polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        claim 2; Page 22-23; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                         and hypercoagulation, e.g. stroke
                             (first entry)
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98US-0087585

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Mismatches:
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121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180 1 GCCAACTCCTTCCTGGAGGAGCTCCGTCAGGAGCCTGGAGGGGGGGAGTGCATAGAGGAG 60 181 AGCCTGTGCTGCGGGCACGGCACGTGCATCGACGGCATCGGCAGCTTCAGCTGCGACTGC .09-763-153-1 (1-1245) x AAY56803 (1-415) 61 g Ω g á g ογ

Human mature wild type protein C.

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GGTGAGGGCTGTGGGCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTC 1200
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301 GACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGCGCTGTAGCTGT 360
          841 AGGGCCTTGCAGAGCGCGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGG
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serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; alcisseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorthagic fever; protein C defictency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
protein C derivative; anticoagulation activity; thrombosis;
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WO200159084-A1.

16-AUG-2001

02-FEB-2001; 2001WO-US01221.

11-FEB-2000; 2000US-0181948. 14-MAR-2000; 2000US-0189199;

(ELIL ) LILLY & CO ELI.

Grinnell BW, Jones BE; Gerlitz BE,

WPI; 2001-514662/56. N-PSDB; AAD15223. Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions

Claim 1; Page 43-44; 59pp; English.

molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a infarction and unstable angina; and disease states predisposing to thrombosis; vascular occlusive disorders and hypercoagulable states e.g. thrombosis; vascular occlusive disorders and hypercoagulable states e.g. thalassaemia, sickle cell disease, viral heemorrhagic fever and permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial with an anti-platelet agent; protein C deficiency; acute arterial or peripheral arteries or in vascular grafts in combination with a thrombotytic agent. Nuclein call grafts in combination with a containing humans with genetically predisposed prothrombotic disorders of for treating humans with genetically predisposed prothrombotic disorders or for treating humans with genetically predisposed prothrombotic disorders protein C. The invention relates to human protein C derivatives and nucleic acid

Alignment Scores:

419 415 0 0 0 Conservative: Mismatches: Length: Matches: Indels: Gaps: 1.34e-159 2298.00 100.00% 100.00% 98.33**%** 22 Best Local Similarity: Percent Similarity: Query Match:

US-09-763-153-1 (1-1245) x AAE08625 (1-419)

- 1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCCTGGAGCGGGAGTGCATAGAGGAG 60
- 61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120 δ

21 IleCysAspPheGluGluAlaLysGluIlePheGlnAsnValAspAspThrLeuAlaPhe 40

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Domain

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The present sequence is that of human protein C mature polypeptide. The invention relates to human protein C derivatives having at east 2 amino acid substitutions, and to recombinant DNA molecules encoding such derivatives. These derivatives have increased anticoagulant activity and resistance to inactivation by serpins activity of the wild-type human protein. Out retain the biological activity of the wild-type protein. The amino acid substitutions are selected from H100, S116, S12K, Q32E, N33D, N33F, and amino acids at collypeptide substituted with Ser, Ala, Thr, H1s, Lys, Leu, Arg, Asn, Asp, G1u, Gly or Gln. Preferred protein C derivatives are protein c polypeptide substituted with Ser, Ala, Thr, H1s, Lys, Leu, Arg, Asn, Asp, G1u, Gly or Gln. Preferred protein C derivatives are encoding the novel human protein C derivatives, transformed host encoding the novel human protein C derivatives are used of sease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina), vascular occilusive myocardial infarction and unstable supers, sepsis (in combination with activatives are desired protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an entitlement), protein C deficiency, acute arterial thrombotic catheter), protein C deficiency, acute arterial thrombotic catheter), protein C deficiency, acute arterial thrombotic certebral or peripheral arteries or in vascular grafts. Human patients with companients or in vascular genetically predisposed prothrombotic disorders may be treated by genetically predisposed prothrombotic disorders may be treated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AGCCTGTGCTGCGGGCACGGCACGTGCATCGACGCATCGGCAGCTTCAGCTGCGACTGC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism -
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                                                                       02-FEB-2000; 2000US-0179801.
14-MAR-2000; 2000US-0189197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.33%
                                                                                                                                  (ELIL ) LILLY & CO ELI.
                                                                                                                                                                             Jones BE;
                                                                                                                                                                                                                 WPI; 2001-496919/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity:
                                                                                                                                                                                                                                      N-PSDB; AAH26361.
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09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "cleavage makes a 2-chain inactive
precursor (155-amino acid light chain
attached via a disulfide bond to a
262-amino acid heavy chain)"
                                                                                                                                                                                                                                                                                                 myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy.
                                                                                                                                                                                                                                                                                    Protein C; human; coronary syndrome; thrombosis; angina;
        1201 GACTGGATCCATGGGCACATCAGAGACAAGGAAGCCCCCCAGAAG 1245
                           'note= "thrombin cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "gamma-carboxylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "0-phosphorylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1..45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note- "Gla domain"
                                                                                                                          AAB82673 standard; Protein; 419 AA.
                                                                                                                                                                                                            15-OCT-2001 (first entry)
                                                                                                                                                                                                                                                  Wild-type human protein C.
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Peptide

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241 CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGTG 300
                                301 GACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGGTGTAGCTGT 360
                                                                        GCGCCTGGCTACAAGCTGGGGGACGACTCCTGCAGTGTCACCCCCCAGTGAAGTTCCCT 420
                                                                                                                                              421 TGTGGGAGGCCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGACACAGAA 480
                                                                                                                                                                                      481 GACCAAGAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGGGGAGAC 540
                                                                                                                                                                                                  61 SerLeuCysCysGlyHisGlyThrCysIleAspGlyIleGlySerPheSerCysAspCys 80
                                                                                                                                                                                                                              541 AGCCCTGGCAGGTGGTCCTGGTGGACTCAAAGAAGAAGCTGGCCTGCGGGGGAGTGCTC 600
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The present invention relates to a human protein C derivative. The protein is useful for treating vascular occlusive disorders.

Typercogalable states such as sepsis, disseminated intravascular coagulation, purpura fulminans, major tramam, major surgery, burns, coagulation, purpura fulminans, major tramama, major surgery, burns, thrombosis, hepatin-induced thrombocytopenia, sickle cell disease, thalassemia, viral hemorrhagic fever, thrombotic thrombocytopenic thromboty districts and hemolytic uremic syndrome, and also useful for treating infarction, unstable angina, and stroke. Protein C derivatives with infarction and substitutions result in increased resistance to inactivation by septins when compared to wild-type activated human creduire either less frequent administration and/or smaller dosage than wild type human protein C for treating disorders.
                                                                                                                                                                                                                                                                                                                                                                                                      Protein C derivatives, useful for treating vascular occlusive disorder, hypercoagulable state, thrombotic disorder and disease states predisposing thrombosis, comprises specific amino acid substitutions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AICTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TGGICCAAGCACGICGACGGIGACCAGIGCITGGICIIGCCCIIGGAGCACCCGIGCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACGAGCCTGGAGCGGGAGTGCATAGAGGAG
                                                                                              Protein C; human; vascular occlusive; burn; transplantation; deep vein thrombosis; sickle cell; thalassemia; thrombotic disorders; myocardial infarction; angina; stroke.
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 42-44; 57pp; English.
                                                                      Human protein C derivative 1.
                                                                                                                                                                                                                                                                          99US-0131801.
                                                                                                                                                                                                                                             13-APR-2000; 2000WO-US08722.
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2298.00
100.00%
100.00%
98.33%
                                            (first entry)
                                                                                                                                                                                                                                                                                                    (ELIL ) LILLY & CO ELI.
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                                                                                                                                                                                     WO200066754-A1.
                                                                                                                                                           Homo sapiens.
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                                          26-FEB-2001
                                                                                                                                                                                                                                                                          30-APR-1999;
                                                                                                                                                                                                                  09-NOV-2000.
                                                                                                                                                                                                                                                                                                                                   Gerlitz BE,
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                AAB36894;
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AAB36894 standard; Protein; 419 AA.

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1141 GGTGAGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTC 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 ValArgLeuGlyGluTyrAspLeuArgArgTrpGluLysTrpGluLeuAspLeuAspIle 240
                                                                                                                                                                                                                                                                                                GACCAAGAAGACCAAGTAGATCCGCGCCTCATTGATGGGAAGATGACCAGGCGGGGAGAC 540
                                                                                                                                                                                                                                                                                                                             161 AspGlnGluAspGlnValAspProArgLeuIleAspGlyLysMetThrArgArgGlyAsp 180
                                                                                                                                                                                            421 TGTGGGAGGCCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGACACACAGAA 480
                                                                                                                                                                                                                                                   GACAACGCCGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGCTGTAGCTGT 360
                                                                                                                                               101 AspAsnGlyGlyCysThrHisTyrCysLeuGluGluValGlyTrpArgArgCysSerCys 120
                                                       CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG 300
              601 ATCCACCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTT
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181 AGCCIGIGCIGGGGCACGGGACGIGCAICGACGGCAICGGCAGCIICAGCIGCGACIGC
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The invention relates to a conjugate (I) comprising at least one non-compropertied moiety (II) (e.g. an N-glycosyl group) covalently attached to polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one comprising an introduced and/or at least one removed amino acid residue comprising a cattachment group for the non-polypeptide group (e.g. an N-glycosylation cattachment group included are (1) a variant (IV) of (III) comprising a site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the proviso the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln (C) a mucleotide sequence (Y) encoding tis/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (Y) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (C); (1) and the serum half-life of a parent protein C polypeptide.

C (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) (C) increasing (M) the functional in vivo half-compising (V) or (VI); (5) increasing (M) the functional in vivo half-compignates, and in the manufacture of medicaments for the treatment (and medicaments, and in the manufacture of medicaments for the treatment compignation (DIC); sepsis, septic thrombosis, disseminated intravascular coagulation (DIC); sepsis, septic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group
                                                                                                                                                                                 Human; Protein C; N-glycosylation; APC; activated protein C; zymogen; serum half-life; chromosome 2q13-q14; stroke; myocardial infarction; after venous thrombosis; disseminated intravascular coagulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coagulant; adult respiratory distress syndrome; alpha-1 antitrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andersen KV, Pedersen AH, Freskgaard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Activation_peptide
158..419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Lys_Arg_dipeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                            /label- Light_chain
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                AAU99002 standard; Protein; 419 AA.
                                                                                                                                                         Human Protein C zymogen protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MAXY-) MAXYGEN APS.
(MAXY-) MAXYGEN HOLDINGS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-2000; 2000DK-0001560.
18-OCT-2000; 2000US-242268P.
21-JUN-2001; 2001DK-0000970.
21-JUN-2001; 2001US-300154P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-OCT-2001; 2001WO-DK00679.
                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200232461-A2
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                        23-AUG-2002
                                                                              AAU99002;
                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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RESULT 5
                        AAU99002
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cc shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an antitrypsin. The conjugates have an increased in vivo half-life, and alpha-1 increased serum half-life, increased resistant to inhibitors, reduced conjugate offers an unmber of advantages over the currently available. The conjugate offers a number of advantages over the currently available of APC products, including longer duration between injections, cadministration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of cativated protein C) conjugates. This must be especially important when conjugate has an extended plasma life. The gene for protein C is protein C upon which the variants of the invention were based.
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Sequence 419 AA;

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961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCT 1020
661 GTCAGGCTTGGAGATATGACCTGCGGCGCTGGGAGAGTGGGGAGCTGGACCTGGACATC 720
         721 AAGGAGGICTICGICCACCCCAACTACAGCAAGAGCACCACCGACAATGACATGGCACTG 780
                                                781 CIGCACCIGGCCCAGCCGCCACCTCICGCAGACCAIAGIGCCCATCIGCCICCCGGAC 840
                                                                                                                                                                                                                                 1021 GAGAACAIGCIGIGIGCGGGCAICCICGGGGACCGGCAGGAIGCCIGCGAGGGCGACAGI 1080
                                                                                                                                                                                                                                                                      1081 GGGGGCCCATGGTCGCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGG 1140
                                                                                                                                                                                                                                                                                                             1141 GGTGAGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTC 1200
                                                                                      841 AGCGGCCTTGCAGAGGGGGAGCTCAATCAGGCGGGCCAGGAGCCCTCGTGACGGGCTGG 900
                                                                                                                         901 GGCTACCACAGCAGCGAGAGAAGAGGCCCAAGAAAACGGCACCTTCGTCCTCAACTTC 960
                                                                                                                                                                                                       The human protein C is expressed in large amts. using plasmid pPC 1 in E.coli K12/Om 225 (FERM P-9297).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein C gene - prepd. from new DNA of specified base sequence.
                                                                                                                                                                                                                                                                                                                                                  1201 GACTGGATCCATGGGCACATCAGAGAACAAGGAAGCCCCCCAGAAG 1245
                                                                                                                                                                                                                                                                                                                                                             AAP81104 standard; protein; 460 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein C; plasmid pPC 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; ; 16pp; japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of human protein C.
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N-PSDB; AAN81408.
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901 GGCTACCACAGCAGCCGAGAGGAGGGCCAAGAGAAACCGCACCTTCGTCCTCAACTTC 960
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95US-0565074.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PPLT-) PPL THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Foster
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                                                                                                                                                                                                                                                                                                                                    Human protein C.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            661 GTCAGGCTTGGAGAGTATGACCTGCGGCGGGAGAGAGTGGGAGCTGGACCTGGACATC 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 ValargLeuGlyGluTyrAspLeuArgArgTrpGluLysTrpGluLeuAspLeuAspIle 281
                                                                                                                                                                                                                                                                                                                                                                                        GCGCCTGGCTACAAGCTGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT 420
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                                                                                                                                                                                                                                                                  181 AGCCTGTGCTGCGGCCACGCCACGTGCATCGACGCCATCGGCAGCTTCAGCTGCGACTGC 240
                                                                                                                                                                                                                                                                              .21 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCCTGCGCC 180
                                                                                                                                                                                                                                       61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
                                                                                                                                               9
                                                                                                                                                                                               62 IleCysaspPheGluGluAlaLysGluIlePheGlnAsnValAspAspThrLeuAlaPhe 81
                                                                                                                                                          42 AlaAsnSerPheLeuGluGluLeuArgHisSerSerLeuGluArgGluCysIleGluGlu 61
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                                                                   Matches:
                                                                                                  Indels:
                                                        Length:
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                                                          1.37e-159
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100.00%
98.33%
                                                                                          Best Local Similarity:
                               460 AA;
                                                                               Percent Similarity:
                                                   Aliqnment Scores:
                                Sednence
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1141 GGTGAGGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTC 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This polypeptide comprises human protein C. A claimed method for producing recombinant human protein C in the milk of a transgenic animal involves: (a) providing a DNA construct comprising DNA encoding a secretion signal and a protein C propeptide, operably linked to DNA encoding the construct of the 2 DNA sequences being linked to elements required for protein C expression in a mammary gland of a host female animal; and (b)
                                                           961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCT 1020
                                                                                                                                                                                                                                                                                                                                                              Protein C; transgenic animal; sheep; rabbit; cattle; goat; milk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Production of protein C in transgenic animal - useful for high
quantity protein C production with therapeutic value
                                                                                                                                                                                                                                                                                                                                                                                                                                 1201 GACTGGATCCATGGGCACATCAGAGACAAGGAAGCCCCCCAGAAG 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garner I, Prunkard DE;
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/note= "two-chain cleavage site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         blood clotting; anticoagulant; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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using the DNA construct to breed a transgenic animal (esp. sheep, rabbit, cattle, goat) that produces protein C in its milk, at least 90% of the protein C being in the two-chain form. Modification of the protein C two-chain cleavage site (see AAW25085) improves the maturation of recombinant protein C from single chain to two-chain form.
                                                                                                                                                                                                                                                                          61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
                                                                                                                                                                                                                                                                                                                        121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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The claimed sequence AAN60001 has "RIN-RM" attached to its 5' end wherein: R= AAN60002 or AAN60003; and R1= AAN60004 or AAN60005; and M and
                                                                                                     961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCT 1020
                                                                                                                                              1021 GAGAACATGCTGTGCGGGCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGCGACAGT 1080
                                                                                                                                                                                       1081 GGGGGCCCATGGTCGCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGG 1140
                                                                                                                                                                                                                                1141 GGTGAGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTC 1200
303 LeuHisLeuAlaGlnProAlaThrLeuSerGlnThrIleValProIleCysLeuProAsp 322
                    841 AGCGGCCTTGCAGAGGGGGGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGG 900
                                901 GGCTACCACAGCAGCCGAGAAGGAGGCCCAAGAAACCGCACCTTCGTCCTCAACTTC 960
                                                                        Prodn. of polypeptide having human protein C activity - is brecombinant DNA procedures for prod. useful against vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beckmann RJ, Jaskunas SR, Lai MHT, Little SP;
Santerre RF;
                                                                                                                                                                                                                                                                         1201 GACTGGATCCATGGGCACATCAGAGACAAGGAAGCCCCCCCAGAAG 1245
                                                                                                                                                                                                                                                                                     Sequence of polypeptide with human protein C activity.
                                                                                                                                                                                                                                                                                                                                                                                                                        Vascular disorder therapy; protein C deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note='"encoded by AAN60004"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86EP-0300823.
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/note= "€
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-FEB-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            601 ATCCACCCTCCTGGGTGCTGACAGGGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTT 660
                                                                                                                                                                                                                                                                                                                                                                                                               GACCAAGAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGGGAGAC 540
                                                                                                                                                                                                                                                                                                                                                      541 AGCCCCTGGCAGGTGGTCCTGGTGGACTCAAAGAAGAAGCTGGCCTGCGGGGCCAGTGCTC 600
                                                                                                                                                                                                                                                                                                                                                                                  421 TGTGGGAGGCCCTGGAAGGGGGATGGAGAAGGAGCGCAGTCACCTGAAACGAGACACAGAA 480
                                                                                                                                                                                                                                                                                                                         GACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGCTGTAGCTGT 360
                                                                                                                                                                                                                                                                  CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG 300
                                                                                                                                                                                                                                   N= 0 or 1; provided that when M=0, N=0; and that when R= AAN60002, R1=AAN60004; and that when R= AAN60003, R1= AAN60005.
                                                                                                                                       61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
                                                                                                                                                                    121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
                                                                                                           1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCCGGAGGGGGGAGTGCATAGAGGAG 60
                                                                                                                   Conservative:
                                                                     Mismatches:
                                                      Matches:
                                                                           Indels:
                                               Length:
                                                                                   Gaps:
                                                                                               US-09-763-153-1 (1-1245) x AAP60001 (1-461)
                                                1.37e-159
                                                     2298.00
100.00%
100.00%
98.33%
                          461 AA;
                                                                    Best Local Similarity:
Query Match:
                                                                Percent Similarity:
                                           Alignment Scores:
                            Seguence
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1081 GGGGGGCCCATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGG 1140
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                                                                                                                                       1021 GAGAACHTGCTGTGTGCGGGCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGCGACAGT 1080
                                                                                 961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCT 1020
                                                                                                                                                                                                             323 SerGlyLeuAlaGluArgGluLeuAsnGlnAlaGlyGlnGluThrLeuValThrGlyTrp 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "links together the two processed chains"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "apparent processing site for connecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59..64
60..63
/label= gamma-carboxyglutamic acid (Gla) domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "in heavy chain; converts to activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human Protein C; anti-coagulant; thrombosis; serine protease.
                                                                                                                                                                                                                                                                                                             1201 GACTGGATCCATGGGCACATCAGAGACAAGGAAGCCCCCCAGAAG 1245
                                                                                                                                                                                                                                                                                                                            growth factor domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= prepro leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= N-glycosylation site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  AAP70855 standard; Protein; 461 AA.
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162..175
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Disulfide-bond
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Murray MJ, Berkner KL, Foster DC, Davie
  Cleavage-site
         EP215548-A.
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/note= "apparent processing site for connecting
dipeptide
                                               dipeptide"
                                                                                                                                                                  85US-0749600.
85US-0766109.
                                                                                                                                       86EP-0304970.
                                                                                                                                                                                                                                 (UNIW ) UNIV OF WASHINGTON.
           199..200
                                                                                                                                                                                                                  (ZYMO-) ZYMOGENETICS INC.
                                                                                                                                    26-JUN-1986;
                                                                                                                                                                                  15-AUG-1985;
                                                                                                    25-MAR-1987
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Human protein C or activated protein C - prepd. using expression vector capable of integration in mammalian host cell DNA WPI; 1987-081505/12. N-PSDB; AAN70102

Claim 4; Fig 4; 52pp; English.

Recombinantly produced protein C can be used to treat thrombotic disorders such as venous thrombosis as it has anti-coagulant properties. The protein sequence is thought to yield two peptide chains; the first contains the Gla domain and growth factor domains and the second (the activation peptide) contains the catalytic

461 AA; Sequence

461 415 0 0 0 Matches: Conservative: Mismatches: Indels: Length: 1.37e-159 2298.00 100.00% 100.00% 98.33% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB:

US-09-763-153-1 (1-1245) x AAP70855 (1-461)

61 AICIGIGACTICGAGGAGGCCAAGGAAATTITCCAAAAIGIGGAIGACACACTGGCCTTC 120 .21 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180 181 AGCCTGTGCGGGGACGGCACGTGCATCGACGGCATCGGCAGCTTCAGCTGCGACTGC 240 241 CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG 300 301 GACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGGTGTAGCTGT 360 361 GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTACCCCCGCAGTGAAGTTCCCT 420 1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACCAGCCTGGAGCGGGAGTGCATAGAGGAG 60 δ g g ŏ ö q ŏ g g à ŏ

EP323149-A.

421 TGTGGGAGGCCCTGGAAGCGGATGGAGAAGGAGCGCAGTCACCTGAAACGAGACACAGAA 480 541 AGCCCTGGCAGGTGCTGGTGGACTCAAAGAAGAAGCTGGCCTGCGGGGCAGTGCTC 600 961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCT 1020 661 GTCAGGCTTGGAGATATGACCTGCGCGCTGGGAGAGTGGGAGCTGGACCTGGACATC 720 1021 GAGAACAIGCIGIGIGGGGCAICCICGGGGACCGGCAGGAIGCCIGCGAGGGGGGACAGI 1080 1081 GGGGGCCCATGGTCGCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGG 1140 AAGGAGGTCTTCGTCCACCCCAACTACAGCAAGAACACCACCGACAATGACATCGCACTG 780 781 CIGCACCIGGCCCAGCCGCCACCCICTCGCAGACCATAGIGCCCATGTGCCTCCCGGAC 840 841 AGCGCCCTTGCAGAGCGCGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGG 900 1141 GGTGAGGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTC 1200 GGCTACCACAGCAGCGAGAGAAGGAGAGAGAAAACGGCACCTTCGTCCTCAACTTC 960 601 ATCCACCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTT Human protein C; zymogen form; activated C protein; human liver mRNA; signal peptide; propeptide; antithrombotic. 1201 GACTGGATCCATGGGCACATCAGAGACAAGGAAGCCCCCCAGAAG 1245 AAP90401 standard; protein; 461 AA. Zymogen form of human protein C. 01-NOV-1989 (first entry) Homo sapiens 901 ò α δ g ð ò g ŏ Db δ g ŏ g ò ద ò q οŽ g ŏ qq δý g g δ 

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activation.
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Grinnell BW, Yan SB;
                         88EP-0312201.
                                                   87US-0138009.
                                                                                 (ELIL ) ELI LILLY AND CO.
                                                                                                            Ehrlich HJ,
                                                                                                                                      1989-194452/27.
                                                                                                                                                     N-PSDB; AAN90187
                         22-DEC-1988;
                                                      28-DEC-1987;
05-JUL-1989.
                                                                                                              Bang NU,
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New DNA encoding zymogen form of human protein C - and its activated deriv., useful as eg antithrombotic agents more sensitive to thrombin

Disclosure; page 4 - 7; 65pp; English.

This is the protein sequence of nascent human protein C encoded by the DNA of AAN90187, which is derived from cDNA clones prepd. from human liver mRNA. It comprises the following regions: residues 1-42 are the signal peptide and propeptide of human protein C, important for directing secretion and propeptide of human protein C, important for directing secretion and protein C, insolutes 43-197, once post-cranslationally modified, constitute the light chain of both two-chain zymogen and activated forms of protein C; residues the two-chain zymogen and activated forms of protein C; residues 50 be removed (on basis of homology with 50 bovine protein C) probably by a 2 step process comprising a bovine protein C) probably by a 2 step process comprising a first cleavage (either between residues 197-8 or 199-200), first cleavage (either between residues 197-8 or 199-200), followed by carboxypeptidase or aninopeptidase action, to form 2 followed by carboxypeptidase or aninopeptidase action, to form 2 chain protein C; residues 200-211 constitute the activation activated heavy chain of the 2 chain form of protein C zymogen, once 3 modified, constitute the activated heavy chain of the 2 chain form of protein C zymogen, once 3 protein C zymogen and activated heavy chain and activated he Protein C zymogen and activated protein C are regulators of haemostasis, differing from native protein C by increased sensitivity to activation by thrombin and thrombin/ thrombomodulin (even in presence of Ca ions) and longer in vivo half life. They are useful as on-demand antithrombotic agents, (replacements for heparin and hydroxycoumarins) and for treatment of hereditary protein C deficiency states.

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Sequence

461 415 0 0 0 0
. Length: Matches: Conservative: Mismatches: Indels: Gaps:
1.37e-159 2298.00 100.00% 100.00% 98.33%
Alignment Scores: Pred. No.: Score: Ccent Similarity: t Local Similarity: iry Match:

US-09-763-153-1 (1-1245) x AAP90401 (1-461)

	09	62	120	82	180	102	240	122	9
20000	1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCCAGCCTGGAGCGGGGGTGCATAGAGGGG 60	43 AlaAsnSerPheLeuGluGluLeuArgHisSerSerLeuGluArgGluCysIleGluGlu 62	61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120		121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC	03 mrncariveHisValAspGlyAspGlnCvsLeuValLeuProLeuGluHisProCysAla	of informal distributions of the composition of the	AGCCTGTGCTGCGGGCACGCCACGTCACGCATCGCCATCGCCATCGCTTCTTTTTTTT	103 SerLeuCysCysGlyHisGlyThrCysIleAspGlylleGlySerFneSerCysAspCys 122
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1081 GGGGGGCCCATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGACTGG 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCT 1020
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                                             421 TGTGGGAGGCCCTGGAAGCGGATGGAGAAGCGCAGTCACCTGAAACGAGACACAGAA 480
                                                                                                                     781 CIGCACCIGGCCCAGCCCGCCACCTCGCAGACCATAGIGCCCATCIGCCTCCCGGAC
                                                                                                                                                                                                                                                                                                                                              661 GTCAGGCTTGGAGGTATGACCTGCGGCGCTGGGAGAAGTGGGAGCTGGACCTGGACATC
                                                                                                                                                                                                                        601 ATCCACCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTT
                                                                                                                                                481 GACCAAGAACAAGTAGATCCGCGCTCATTGATGGGAAGATGACCAGGCGGGGAGAC
                                                                                                                                                                                    541 AGCCCCTGGCAGGTGGTCCTGCAGACTCAAAGAAGAAGCTGGCCTGCGGGGCAGTGCTC
                                                                                                                                                                                            241 CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG
                                   301 GACAACGGCGGCTGCACGCATACTGCCTAGAGGAGGTGGGGCTGGCCGCCTGTAGCTGT
                                                                       361 GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCCGCAGTGAAGTTCCCT
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'label = N-glycosylation site
                                                                                                                                                                                                                                                                                      /label= N-glycosylation site
                                                                                                                /label= activation peptide
                                                                    label= pre-pro peptide 3..197
                                                         Location/Qualifiers
                                                                                label= light chain
                                                                                                                            'label= heavy chain
                                                                                                                                       /label= Gla domain
                                Anticoagulant; fibrinolysis.
            (first entry)
                                                                                                                                                                                                                                                                                                                       90WO-US07617.
                                                                                                                                                                                                                                                                                                                                  89US-0456092.
                                                                                     .198
                                                                                                 . 200
                                                                                                                       .461
                                                                                                                                                                                                                                                                                                                                                  (ZYMO-) ZYMOGENETICS INC.
                      Protein C precursor.
                                                                                                                                                                                                                                                                                                                                                             Foster DC, Holly RD,
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-222903/30.
                                                                                                                                                                                                                                                                                                                                            (TEIJ ) TEIJIN LTD
                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ12649
                                                                                   Cleavage-site
                                                                                              Cleavage-site
                                                                                                                                          Modified-site
                                                                                                                                                     Modified-site
           02-OCT-1991
                                             Homo sapiens
                                                                                                                                                                 Modified-site
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                                                                                                                                                                                                                                                                                                                      21-DEC-1990;
                                                                                                                                                                                                                                                                                                                                 22-DEC-1989;
                                                                                                                                                                                                                                                                                                WO9109951-A
AAR13074;
                                                                                                                                                                                                                                                                                                           11-JUL-1991
                                                             Peptide
                                                                                                         Peptide
                                                                         Region
                                                                                                                     Region
                                                                                                                                Domain
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The sequence was deduced from a clone isolated from a CDNA library prepd. from mRNA from Hep G2 cells. It is a protein C precursor, including light and heavy chains, which is cleaved to produce activated protein C (see feature table). The DNA encoding the sequence can be manipulated by genetic engineering techniques to express a protein comprising (when activated) a heavy chain and a truncated light chain comprising residues 1-149, 1-150, 1-151 or 1-10.
                                                                                                                                               Pre-pro = pre-pro peptide of protein C with all/part replaced by the corresponding peptide of either protein S, factors VII, IX or X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 IGGICCAAGCACGICGACGGIGACCAGIGCTIGGICTIGCCCTIGGAGCACCCGIGCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AGCCIGIGCIGCGGGCACGGCACGIGCAICGACGGCAICGGCAGCIICAGCIGCGACIGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 GACAACGGCCGGCTGCCACGCATTACTGCCTAGAGGAGGTGGGGCTGGCGGCGCTGTAGCTGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCCTGGAGCGGGAGTGCATAGAGGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGGAGTGAAGTTCCCT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 TGTGGGAGGCCCTGGAAGGGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGACAAGAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 GACCAAGAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGGGGAGAC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H = heavy chain.
Cells transformed with expression vectors contg. the modified DNA sequences produce the new proteins which can be used to regulate anticoagulant and fibrinolytic systems.
See also W09112320 (AAR13074).
                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                                                             or prothrombin, L = AAs 1-149, 150, 151 or 152 of light chain,
                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                Matches:
                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-763-153-1 (1-1245) x AAR13074 (1-461)
                                                                                                                                       Pre-pro-L-X-H
                                                                                                                                                                                                      = 3-10 Lys/arg residues; and
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Best Local Similarity:
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                                                                                                                                                                                                                 /label= proteclytic cleavage
                                                                                                                                                                                                                                               /label= proteolytic cleavage
201...211
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Disclosure; Fig 1; 60pp; English.

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1141 GGTGAGGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTC 1200
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                                                                                                                                                                                                                                                   1081 GGGGGGCCCATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGG 1140
                                                                                                                                                                                       961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCT 1020
                                                                                                                                                                                                                                                                                           901 GGCTACCACAGCAGCCGAGAGAAGGAGGCCAAGAGAAACCGCACCTTCGTCCTCAACTTC 960
                                                             721 AAGGAGGTCTTCGTCCACCCCAACTACAGCAAGAGCACCACCGACAATGACATGGCACTG 780
                                                                                                     841 AGCGGCCTTGCAGAGCGCGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGG 900
                                                                                                                                  661 GTCAGGCTTGGAGAGTATGACCTGCGGCGCTGGAGAAGTGGGAGCTGGACCTGGACATC 720
                                        243 IlenisproserTrpvalLeuThrAlaalaHisCysMetAspGluSerLysLysLeuLeu 262
                                                                                                                                                                                                                                                                                                                                                                                                                             Phopholipid; binding protein; lipocortin; domain; vitamin K; PBP;
                                                                                            781 CIGCACCIGGCCCAGCCGCCACCCICTCGCAGACCAIAGIGCCCAICTGCCICCCGGAC
  601 ATCCACCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTT
                                                                                                                                                                                                                                                                                                                   1201 GACTEGATCCATGGGCACATCAGAGACAAGGAAGCCCCCCAGAAG 1245
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/label- mat_protein
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481 GACCAAGAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGGGGAGAC 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 AlaProGlyTyrLysLeuGlyAspAspLeuLeuGlnCysHisProAlaValLysPhePro 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 TGTGGGAGGCCCTGGAAGCGGATGGAGAAGAGGGCAGTCACCTGAAACGAGACACAGAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence, or a fragment of it, is used in the construction of hybrid phospholipid-binding proteins (PBP) having the same biological activity as human protein C or human activated protein C. The hybrid sequence would comprise at least one lipocortin phopholipid binding domain (PBD), e.g. of PAP-I, joined to a gla-domainless protein C or activated protein C. See AAQ12680-81 for such examples. See also AAQ12678-81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 AGCCIGTGCTGCGGGCACGGCACGTGCATCGGCATCGGCAGCTTCAGCTGCGACTGC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 GCGCCTGGCTACAAGCTGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT
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                                                                                                 Recombinant prodn. of hybrid phospholipid-binding proteins comprising lipocortin phospholipid-binding domain and
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Mismatches:
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Matches:
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                                                                                                                                                                         Disclosure; Fig 2; 57pp; English.
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100.00%
100.00%
98.33%
                                                                                                                                        vitamin K-dependent protein
(ZYMO-) ZYMOGENETICS INC.
                                                              WPI; 1991-222905/30.
                                                                                                                                                                                                                                                                                                                                         Sequence 461 AA;
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                                                                                   N-PSDB; AAQ12678
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                                    Foster DC;
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601 ATCCACCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTT 660
        661 GTCAGGCTTGGAGGTATGACCTGCGGCGCTGGGAGAAGTGGGAGCTGGACCTGGACATC 720
                                        721 AAGGAGGICITCGICCACCCCAACTACAGCAAGAGCACCACCGACAATGACATCGCACTG 780
                                                                          781 CTGCACCTGGCCCAGCCGCACCTCTCGCAGACCATAGTGCCCATCTGCCTCCCGGAC 840
                                                                                                                                                                                                 961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCCGAGGTCATGAGCAACATGGTGTCT 1020
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                                                                                                          1081 GGGGGCCCATGGTCGCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGG 1140
                                                                                                                                841 AGCGGCCTTGCAGAGCGCGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGG 900
                                                                                                                                         901 GGCTACCACAGCAGCCGAGAAGGAGGCCAAGAAACCGCACCTTCGTCCTCAACTTC 960
                                                                                                                                                                         1141 GGTGAGGGGTGTGGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTC 1200
                                                                                                                                                                                                           1201 GACTGGATCCATGGGCACATCAGAGAAGAAGCCCCCCAGAAG 1245
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/note= "Light chain, see comment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= signal peptide
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                                                                                                                                                                                                                                                                                                                                                                                 AAR13622 standard; Protein; 461 AA.
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61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGGAGGTGAGCTTCCTCAATTGCTCGCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The amino acid sequence codes for human protein C (HPC). The activated protein can comprise one of 3 different truncated light chains, ADa(1) to Lys(150), Lys(151) or Arg(152). The activated HPC with a truncated light chain is more stabled during storage. It can be administered for prophylactic and/or therapeutic treatments of disease states or injuries to enhance the patient's own anti-coagulative or fibrinolytic capabilities. See also W09109951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT 420
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                                                                                                                                                                                                                                                                                                                                                                   461
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                                                                                                        Miyagi F, Sumi Y, Wakabayashi K, Foster DC;
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Mismatches:
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                                  91WO-US00912.
                                                        90US-0478084.
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                                                                                                                             WPI; 1991-267132/36.
N-PSDB; AAQ13357.
                                                                                       (TEIJ ) TEIJIN LID.
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                              08-FEB-1991;
                                                     09-FEB-1990;
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            22-AUG-1991.
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                                                                                                                                                                     CTGCACCTGGCCCAGCCCGCCACCTCTCGCAGACCATAGTGCCCCATCTGCCTCCCGGAC 840
                                                                                                                                                                              721 AAGGAGGTCTTCGTCCACCCCAACTACAGCAAGAGCACCACCGACAATGACATCGCACTG 780
                                                                                                                                             283 LysGluValPheValHisProAsnTyrSerThrThrAspAsnAsp1leAlaLeu 302
                                          123 SerprofipGlnValValLeuLeuAspSerLysLysLysLeuAlaCysGlyAlaValLeu 242
                                                                  601 ATCCACCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTT 660
                                                                           GTCAGGCTTGGAGAGTATGACCTGCGGCGCTGGGAGAAGTGGGAGCTGGACCTGGACATC 720
                                                                                                             541 AGCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGATGGCTGCGGGGCAGTGCTC 600
481 GACCAAGAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGGGGAGAC 540
        Protein C; heavy chain; light chain; anticlotting; fibrinolysis;
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/label= C-terminal
/note= "light chain"
193..197
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241 CGCAGCGGTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCGTCAATTGCTCGCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ATCIGIGACTICGAGGAGGCCAAGGAAATTITCCAAAATGIGGAIGACACACIGGCCTIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A human protein C or an activated protein C has a H chain contg. one of the residues 239-246 (= residues 450-457 in the sequence below) of hatural activated protein C as the C-terminal, or has a L chain contg. one of the residues 141-155 (= residues 141-155 in the sequence below), pref. residues 149-155 (= residues 149-155 in the sequence below) in the L chain of natural activated protein C in the sequence below) in the L chain of natural activated protein C as the C-terminal. The human protein C or the activated protein C can be used as an anticlotting agent or a fibrinolysis promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCCAACTCCTTCCTGGAGGAGCTCCGTCAACAGCAGCTGGAGGGGAGTGCATAGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                               Human protein C and activated protein C with short H chains useful as anti-clotting agents and fibrinolysis promoters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461
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Mismatches:
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Matches:
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                                                                                                                                                                   /note= "heavy chain"
                                                                                                      /label= C-terminal
/note= "heavy chain"
/label= C-terminal
/note= "light chain"
                                                /label= N-terminal
/note= "heavy chain"
                                                                                                                                                     /label= C-terminal
                                                                                                    C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.37e-159
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                                                                                                                                     451..461
                                                                                    458..461
                                   211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                            (TEIJ ) TEIJIN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                             JP05064588-A.
                                                                                                                                                                                                                                                                             14-AUG-1991;
                                                                                                                                                                                                                                           19-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                            Peptide
                                         Peptide
                                                                                           Peptide
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361 GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT 420
          421 TGTGGGAGGCCCTGGAAGCGGATGGAGAAGCGCAGTCACCTGAAACGAGACAGAA 480
                                            481 GACCAAGAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGGGGAGAC 540
                                                                               601 ATCCACCCCTCGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTT 660
                                                                                                                                                                             GTCAGGCTTGGAGAGTATGACCTGCGGCGCTGGGAGAAGTGGGAGCTGGACCTGGACATC 720
                                                                                                                                                                                     961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCT 1020
                                                                                                                                                                                                               721 AAGGAGGICTICGICCACCCAACTACAGCAAGAGCACCACCGACAATGACAICGCACTG 780
                                                                                                                                                                                                                          781 CIGCACCIGGCCCAGCCGCCACCCICICGCAGACCATAGIGCCCATCIGCCICCCGGAC 840
                                                                                                                                                                                                                                                                                                                                                                                            1021 GAGAACATGCTGTGCGGGGATCCTCGGGGACGGGGAGGATGCCTGCGAGGGCGACAGT 1080
                                                                                                                                                                                                                                                             841 AGCGGCCTTCCAAGGGGGGGGGGTCAATCAGGCCGGCCAGGAAACCCTCGTGACGGGCTGG 900
                                                                                                                                                                                                                                                                                                                                                                                                                               1081 GGGGGCCCATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGG 1140
                                                                                                                                                                                                                                                                                                1141 GGTGAGGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCGGCTACCTC 1200
                                                                                                                                                                                                                                                                                                                        901 GGCTACCACAGCAGCGAGAGAGAGGGCCAAGAGAAACCGCACCTTCGTCCTCAACTTC 960
                                                                                                                                                                                                                                                                                                                                    Activated protein C; serine protease; thrombosis; thrombolytic; fibrinolytic; antithrombotic; blood clotting; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1201 GACTGGATCCATGGGCACATCAGAGGACAAGGAAGCCCCCCAGAAG 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW02600 standard; Protein; 461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1996 (first entry)
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/note= "cleavage site between connecting dipeptide
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or in constructs of the invention"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "residue 200 is replaced by Ala, Ser,
Thr or Gly in constructs of the
invention"
                                                                                                          'note= "forms disulphide bond with Cyslll"
                                                                                                                                              /note= "forms disulphide bond with Cys101"
106
                                                                                                                                                                  /note= "forms disulphide bond with Cys120"
                                                                                                                                                                                                         /note= "forms disulphide bond with Cys106"
                                                                                                                                                                                                                            /note= "forms disulphide bond with Cys122"
                                                                                                                             'note= "fors disulphide bond with Cys105"
                                                                                                                                                                                                                                                                                       /note= "forms disulphide bond with Cys151"
                                                                                                                                                                                     /note= "forms disulphide bond with Cys92"
                                                                                                                                                                                                                                                                                                          'note= "forms disulphide bond with Cys160"
                                                                                                                                                                                                                                                                                                                             //octe= "forms disulphide bond with Cys140"
                                                                                                                                                                                                                                                                                                                                                /note= "forms disulphide bond with Cys147"
                                                                                                                                                                                                                                                                                                                                                                                                         /note= "forms disulphide bond with Cys319"
                                                                                                                                                                                                                                                                                                                                                                                     note "forms disulphide bond with Cys162"
                                                                                                                                                                                                                                                                                                                                                                   'note= "forms disuphide bond with Cys175"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "forms disulphide bond with Cys254"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note" "forms disulphide bond with Cys238"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "forms disulphide bond with Cys183"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "residues 198-199 are replaced by Lys-Lys or Arg-Arg in constructs of the invention"
                                                                                                                                                                                                                                                                   /label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Activated_protein-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= N-glycosylation_site 371
                                                  /label- Pre-pro-peptide
                                                                     /label= Mat_protein
                                 Location/Qualifiers
                                                                                        /label= GLA_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 198..199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 200
                                                                                              Disulfide-bond
                                                                                                                 Disulfide-bond
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Human protein C (AAM02600) is a zymogen of a serine protease that plays an important role in the regulation of blood coagulation and the generation of fibrinolytic activity in vivo. It is synthesised in the liver and processed to a 2-chain molecule, which is itself converted to activated protein C. Protein C activated protein C are useful in the treatment of thrombotic activated protein C are useful in the treatment of thrombotic activated protein C are useful in the protein C are useful in the treatment of thrombotic c, modified role (AAT32795) derived from Hep G2 cells. Variant protein C, modified to improve cleavage between the heavy and light chains of the circulating intermediate, can also be produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA encoding modified forms of opt. activated protein C - and related transformed cells for prodn. of recombinant protein C for use e.g. as an anti-thrombotic agent
                                                                                                                               /note= "forms disulphide bond with Cys 398"
                                     /note= "forms disulphide bond with Cys387"
                                                                                                   /note= "forms disulphide bond with Cys426"
                                                                    //note= "forms disulphide bond with Cys373"
/label= N-glycosylation_site
373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 2A-C; 34pp; English.
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                                                                                                                                                                                                                                                                                                                    90US-0582131.
92US-0987532.
                                                                                                                                                                                                                                                                           85US-0749600.
86US-0924462.
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                                                                                                                                                                                                                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-251006/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 461 AA;
                                                                                              398
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                                                                                                                           Disulfide-bond
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                                   Disulfide-bond
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                                                                                                                                                                                                                                    27-JUN-1985;
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61 ATCIGIGACCTICGAGGAGGCAAGGAAATTTICCAAAAIGIGGATGACACACIGGCCTIC 120
                                                                                                                                                           1 GCCAACTCCTTCCTGGAGGAGGTCCGTCACAGCAGCCTGGAGCGGGAGTGCATAGAGGAG 60
                                                                                                               Conservative:
Mismatches:
      Length:
Matches:
                                                    Indels:
                                                                                 US-09-763-153-1 (1-1245) x AAW02600 (1-461)
        1.37e-159
                2298.00
100.00%
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98.33%
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                                 ercent Similarity:
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                                                       Query Match:
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RESULT 16

121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCCTTGGAGCACCCGTGCGCC 180 

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1081 GGGGGCCCATGGTCGCCTCCTTCCACGCACCTGGTTCCTGGTGGCCCTGGTGACTGG 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1141 GGTGAGGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTC 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1021 GAGAACATGCTGTGTGGGGGATCCTCGGGGACCGGCAGGATGCCTGCGAGGGCGACAGT 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                            961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362
                                                                                                                                                                                                                                                                                                                                                                                                                                                      901 GGCTACCACAGCAGCCGAGAGAAGGAGGCCAAGAAAACGGAACTTCGTCCTCAACTTC 960
                                                                                                                                                                                                                                                                                                                                                                                     841 AGGGGCCTTGCAGAGCGCGAGGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGG 900
                                                                                                                                                                                                                                                                        721 AAGGAGGICTICGTCCACCCAACTACAGCAAGAGCACCACCGACAATGACATCGCACTG 780
                                                                                                                                                                                                                                                                                                                  781 CIGCACCIGGCCAGCCGCCACCTCGCAGACCAIAGTGCCCAICTGCCTCCCGGAC 840
                                                                                                                                                                                                                                                                                                                                                   601 ATCCACCCTCCTGGGTGCTGACAGGGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTT 660
                                                                                                                                                                                                                                                 541 AGCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGCTGGCCTGCGGGGCAGTGCTC 600
                                                                                                                                                                                                                481 GACCAAGAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGGGGGAGAC 540
                                                                                                    361 GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT 420
                                                                                                                                     421 TGTGGGAGGCCCTGGAAGGGGATGGAGAAGAAGGGCAGTCACCTGAAACGAGACACAGAA 480
                                                                                                                                              222
                                301 GACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGGCTGGCGGCGGTGTAGCTGT 360
                                                                           181 AGCCIGIGCIGCGGCACGGCACGIGCAICGACGCCAICGGCAGCTICAGCIGCGACTGC 240
          1201 GACTGGATCCATGGGCACATCACAGACAAGGAAGCCCCCCAGAAG 1245
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Human; coding sequence polymorphism; vascular pathology gene;
Polymorphic site; phenotype correlation; forensic; paternity testing;
medicine; genetic analysis; vascular disease.
                                                                                                                                                                                                                                                                Determination of polymorphisms in genes, especially those identifying predisposition to vascular disease
                                                          Human lecithin cholesterol acyltransferase protein sequence.
                                                                                                                                                                                                                   Lander ES, Daley GQ, Cargill M, Ireland JS, Rozen SG;
                                                                                                                                                                                                  (WHED ) WHITEHEAD INST BIOMEDICAL RES.
       AAY49561 standard; Protein; 461 AA.
                                                                                                                                                                   99WO-US06473.
                                                                                                                                                                                    98US-0054272.
                                          13-JAN-2000 (first entry)
                                                                                                                                                                                                                                     WPI; 1999-620066/53.
                                                                                                                                                                                                                                                N-PSDB; AAZ32180
                                                                                                              Homo sapiens.
                                                                                                                                WO9950454-A2.
                                                                                                                                                                26-MAR-1999;
                                                                                                                                                                                  01-APR-1998;
                                                                                                                                                07-0CT-1999.
                          AAY49561;
AAY49561
ID AAY4
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AA232159 to AA232194 represent reference alleles for specifically claimed nucleic acid sequences from the present invention which comprise plymorphic sites as given in a table in the specification, selected from 92 single nucleotide polymorphisms in which the nucleotide at the reference allele. The nucleic acids, and primers and probes, are used to especially polymorphisms, which may predispose an individual to disease, especially a vascular disease. They can also be used in phenotype analysis. AAV49550 to AAV49573 represent the proteins which correspond to some of the reference alleles. Disclosure; Fig 24; 134pp; English. 461 AA; Lignment Scores: Sequence

Pred. No.: Score: Score: Score: Query Match: DB: US-09-763-15; QY 1 GC UP 61 ATC UP 63 116 UP 63 116 UP 63 117 UP 64 1 ATC UP 121 TGG	Pred. No.: 1.37e-159 Length: 461 Score: 2298.00 Matches: 415 Percent Similarity: 100.00% Conservative: 0 Query Match: 100.00% Mismatches: 0 DB: 20 Gaps: 0	US-09-763-153-1 (1-1245) x AAY49561 (1-461)			61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAAATGTGGAAAATGTAGAAAAAAAA		121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTTGGTAATTTTGGTATTTTTGGTATTTTTGGTATTTTTT		AGCTGTGTGTTCTCCCCAACAAAAAAAAAAAAAAAAAAA		
red	o.: Similar Sal Simi	3-153-1	1 GCCAAC	3 AlaAsn	1 ATCTGT	63 IleCys	1 TGGTCC	83 TrpSer	L AGCCTG		
	Pred, No Score: Percent Best Loc Query Ma DB:	92-60-sn									

qq	103
δ	241 CGCAGCGGCTGGGAGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG 30
ą G	123 ArgSerGlyTrpGluGlyArgPheCysGlnArgGluValSerPheLeuAsnCysSerTen 14
ΟŊ	301 GACAACGCCGCCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGCTGGCGCTGCCTGC
Ω	143 AspasnGlyGlyCysThrHisTyrCysLeuGluGluValGlyTrDhrdarnGreener
οy	361 GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCTCT 42
đ	APPOGLYTYTYSLEUGLYASPASPLeuLeuGlnCysHisProAlaValLysPhePro 18
ΟŊ	GTGGGAGGCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAAAAAA
αΩ	
ΟŊ	3CGGCTCATTGATGGGAAGATGACCAGGCGGGAGACACA
qq	pGlnGluAspGlnValAspProArgLeulleAspGlyLvsMetThrArdArglvlar
Qγ	GCCCTGGCAGGTGGTCCTGCACTCAAAGAAGAAGAAGCTGGCCTGCGGCAGTCGTCACTCAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA
qq	POTENGIONALVALLEULEUASPSETLYSLYSLEUAIACYSGIYAIAEU 24
δŻ	TCCACCCTCCTGGGTGCTGACAGCGGCCCACTGCATGAGTCCAAGAAGCTCCTT 66
qq	eHisProSerTrpValLeuThrAlaAlaHisCysMetAspGluSerLvsIvsIvsIeniten
0y	TCAGGCTTGGAGAGTATGACCTGCGGCGCTGGGAGAGTGGGAGCTGGAAGTTGGAGCTTGGAAGTTGAAGTTGGAAGTTGGAAGTTGGAAGTTGGAAGTTGGAAGTTGGAAGTTGGAAGTTGGAAGTTGGAAGTTGGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTAGAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTGAAGTTGAAGTTAAGT
Op	
Οy	SGAGGTCTTCGTCCACCCAACTACAGCAAGCACACCACCACGAATGAAATGACAACAACTACAACAACAACAACAACAACAACAACAACAA
QQ	
Qy	TGCACCTGGCCCAGCCGCCACCTCTCGCAGACCATAGTGCCCATCTCTCTC
qq	
ΟŊ	26 Camara and Table 20 Canada and Camara and
qq	
δy	CCACAGGCGGAGAGGAGGCGAAGAAACCGAAAACGAAAAACGAAAAACGAAAAAA
Dβ	343 GlyTyrHisSerSerArgGluLysGluAlaLysArgAsnArqThrPheVallanscobe 35
δλ	TCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAAACAATGACAACAACAATGAAAAAAAA
QΩ	FILLILI STASDMetV
δŏ	ATGCTGTGTGCGGGCATCCTCGGGGACCGGCAGGATGCTGCAAAAAAAA
Dp	
Qy	GGGGGCCCATGGTCGCCTCCTTCCACGGCACAAGGTTTCAAAAAAAA
QO	
å	11 COMMANDE CONTRACTOR OF THE STATE OF THE SECTION
Ž ž	141 GGTGGGCTCCTTCACAACTACGGCGTTTACACCAAGTCAGCGCTACCT
an ,	423 GlyGluGlyCysGlyLeuLeuHisAsnTyrGlyValTyrThrLysv
ð i	01 GACTGGATCCATGGGCACATCAGAGAAGGAAGCCCCCCAGAAG 1245
	443 AspTrp11eHisGlyHisTleArgAspLysGluAlapr
RESUL AAE08	T 17 626
	AAE08626 standard; Protein; 461 AA.

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The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and and anticoagulation activity to thrombin activation compared to wild type increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C, and retains the biological activity of the wild type human cortain C protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina; of acute aconary syndromes e.g. myocardial infarction and unstable angina; of disease states predisposing to infarction and unstable angina; of disease states predisposing to thrombosis; vascular coagulation (DIC), burns, transplantations, consembliate activity increasing protein; thrombotic disorders in combination of permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial with an anti-platelet agent; protein C deficiency; acute arterial corpusation, thromboembolism or stenois in coronary, cerebral crembolytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders corpus of the present sequence is human wild type protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions
                                                                                                                                              serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein G deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
                                                                                                                             Human; protein C derivative; anticoagulation activity; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 44-46; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-FEB-2001; 2001WO-US01221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-2000; 2000US-0181948.
14-MAR-2000; 2000US-0189199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerlitz BE, Grinnell BW,
                                                     (first entry)
                                                                                                    Human wild type protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIL ) LILLY & CO ELI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200159084-A1.
                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                       01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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Jones BE;

/label = Mature\_human\_wild type\_protein\_C

/label- Signal\_peptide

Location/Qualiflers

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1021 GAGAACAFGCTGTGTGCGGGCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGCGACAGT 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      841 AGCGGCCTTGCAGAGCGCGGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         661 GTCAGGCTTGGAGAGTATGACCTGCGGCGCTGGGAGAAGTGGGAGCTGGACCTGGACATC 720
                                                                                                                                                                                                                                                                                                                                                                                           481 GACCAAGAAGACCAAGTAGATCCGCGCTCATTGATGGGAAGATGACCAGGGGGGGAGAC 540
                                                                                                                                                                                                                                                                                                                                            421 TGTGGGAGGCCCTGGAAGCGGATGGAGAAGAGCGCAGTCACCTGAAACGAGACACAGAA 480
                                                                                                                                                                                                                                                                                                                                                                   183 CysGlyArgProTrpLySArgMetGluLysLySArgSerHisLeuLySArgAspThrGlu 202
                                                                                                                                                                                                                 301 GACAACGGCGGCTGCACGCATACTGCCTAGAGGAGGTGGGGCTGGCGGCGCTGTAGCTGT 360
                                                                                                                                                                                                                                                              361 GCGCCTGGCTACAAGCTGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT 420
                                                                                                                                                                                                                                                                                                            181 AGCCTGTGCTGCGGGACGCACGTGCATCGACGGCATCGGCAGCTTCAGCTGCGACTGC 240
                                                                                                                                                                     241 CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG 300
                                                                                                           121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
                                                                                                                        61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
                              82
                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             781 CIGCACCIGGCCCAGCCCGCCACCTCTCGCAGACCAIAGIGCCCAICTGCCTCCCGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 ValArgLeuGlyGluTyrAspLeuArgArgTrpGluLysTrpGluLeuAspLeuAspIle
                                                                                                                                                                                                                                                                                                                                                                                                       541 AGCCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGAAGCTGGCGTGCGGGGCAGTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 SerbrofrpGlnValValLeuLeuAspSerLysLysLeuAlacysGlyAlaValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 ATCCACCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTT
                                                                            1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCCAGCCTGGAGGGGGGAGTGCATAGAGGAG
US-09-763-153-1 (1-1245) x AAE08626 (1-461)
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Conservative: Mismatches: Length: Matches:

1.37e-159 2298.00 100.00% 100.00% 98.33%

Similarity:

Best Local S: Query Match:

Percent Similarity:

Alignment Scores:

461 AA;

Indels:

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1081 GGGGGCCCATGGTCGCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGG 1140
                                                                1141 GGTGAGGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTC 1200
/note= "activation peptide; removal activates the
                                                                                                                                                                                                                                 Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occlusive disorder; thypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "cleavage makes a 2-chain inactive
precursor (155-amino acid light chain
attached via a disulfide bond to a
262-amino acid heavy chain)"
                                                                                                     1201 GACTGGATCCATGGGCACATCAGAGGAAGGAAGCCCCCCAGAAG 1245
                                                                                                                'note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "gamma-carboxylated"
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200, 211
                                                                                                                                                                                                                                                                                                                                 /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                            43..461
/label= Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2-chain zymogen"
                                                                                                                                                          AAB82674 standard; Protein; 461 AA.
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       "Gla domain"
                                                                                                                                                                                               15-OCT-2001 (first entry)
                                                                                                                                                                                                                 Wild-type human protein C.
                                                                                                                                                                                                                                                                                                                                                                                                          ..151
..175
..319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                        398,
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                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
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                                                                                                                                                                                                                                                                                                                       Peptide
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The present sequence is that of human protein C prepro-polypeptide.
The invention relates to human protein C derivatives having at least 2 amino acid substitutions, and to recombinant bNA molecules encoding such derivatives. These derivatives have increased encoding such derivatives. These derivatives have increased anticoagulant activity and resistance to inactivation by serpins activity of the wild-type human protein C but retain the biological selected from HIGO, SIIG, SIZK, G12E, N31D, N31F, and amino acids at C polypeptide substituted with Ser, Als, Thr. His, Lys, Leu, Arg, C polypeptide substituted with Ser, Als, Thr. His, Lys, Leu, Arg, C polypeptide substituted with Ser, Als Thr. His, Lys, Leu, Arg, C Asn, Asp, Glu, Gly or Gln (numbering relative to the protein C arive protein sequence). Perfected protein C derivatives are encoding the novel human protein C derivatives, transformed host C given in AAB82675-78. Also claimed are a vector comprising DNA C cells and amethod of producing the human protein C derivatives. C The protein C derivatives are useful for treating coronary consorting infarction and unstable engine), vascular occlusive consorting the human during protein c derivatives of disorders and hypercoagulable states predisposing (in rombination with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycatulat intaiction and unstable states, sepsis (in combination with disorders and hypercoagulable states, sepsis (in combination with partericidal permeability increasing protein or with tissue factor anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with man elementary corrections or the peripheral arteries or in vascular grafts. Human patients with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism -
          211..212
/note= "thrombin cleavage site"
                                                                                                                                                                                                                  /note= "O-phosphorylated"
                                                              /note= "N-glycosylated"
                                                                                                   /note= "N-glycosylated"
                                                                                                                                         /note= "N-glycosylated"
                                                                                                                                                                              /note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 50-52; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                          02-FEB-2000; 2000US-0179801.
14-MAR-2000; 2000US-0189197.
                                                                                                                                                                                                                                                                                                                      19-JAN-2001; 2001WO-US00020.
                                                                                                                                                                                                                                                                                                                                                                                                                 (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-496919/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAH26362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 AA;
                                                                                                                                                                                                                                               WO200157193-A2.
      Cleavage-site
                                        Modified-site
                                                                          Modified-site
                                                                                                                 Modified-site
                                                                                                                                                     Modified-site
                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                       09-AUG-2001
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461 415 0 0 0

Conservative: Mismatches: Indels:

Gaps:

Matches:

1.37e-159 2298.00 100.00% 100.00% 98.33%

Best Local Similarity:

Query Match:

Percent Similarity:

Alignment Scores:

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961 ATCAAGATICCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTT 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                901 GGCTACCACAGCAGCCGAGAGAAGGAGGCCAAGAAACGGCACCTTCGTCCTCAACTTC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                         841 AGGGGCTTTGCAGAGGGGGGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGGCTGG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  781 CIGCACCIGGCCCAGCCACCTCTCGCAGACCAIAGIGCCCAICTGCCTCCCGGAC 840
                                                                                                                                                                                                                                                                                                                                                                                                                                   721 AAGGAGGICITCGICCACCCAACTACAGCAAGAGCACCACCGACAATGACATCGCACTG 780
                                                                                                                                                                                                                                                                                                                                                                                                    263 ValargleuGlyGluTyrAspLeuArgArgTrpGluLysTrpGluLeuAspLeuAspIle 282
                                                                                                                                                                                                                                                                                                                             601 ATCCACCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTT 660
                                                                                                                                                                                                                                                               223 SerProTrpGlnValValLeuLeuAspSerLysLysLysLeuAlaCysGlyAlaValLeu 242
                                                                                                                                                                                                                                                                                              541 AGCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGCTGGCCTGCGGGGCAGTGCTC 600
                                                                                                                                                                                                                                          361 GCGCCTGGGTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT 420
                                                                                                                                                                                                          421 TGTGGGAGGCCCTGGAAGCGGATGGAGAAGCGCAGTCACCTGAAACGAGACACAGAA 480
                                                                                                                                                                    301 GACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGGCTGGGGGCGCGTGTAGCTGT 360
                                                                                                                                              181 AGCCTGTGCTGCGGGACGGCACGTGCATCGACGCCATCGGCAGCTTCAGCTGCGACTGC 240
                                                                                                               241 CGCAGCGGCTGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG 300
                                                                         121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCACGTGCGCC 180
                                                                                 61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
                                                  1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCTGGAGCGGGAGTGCATAGAGGAG 60
                  661 GTCAGGCTTGGAGAGTATGACCTGGGGGGGGGGAGAAGTGGGAAGCTGGAACATC
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The present invention relates to a human protein C derivative. The protein is useful for treating vascular occlusive disorders, control is useful for treating vascular occlusive disorders, control is useful for treating as sepsis, disseminated intravascular protein, purpura fulminans, major tranma, major surgery, burns, coaquiation, purpura fulminans, major transplantation, deep vein adult respiratory distress syndrome, transplantation, deep vein corpuration, viral hemorrhagic fever, thrombotic thrombotycopenic thalassemia, viral hemorrhagic fever, thrombotic thrombotycopenic chrombotic disorders and acute coronary syndromes such as myocardial infarction, unstable angina, and stroke. Protein C derivatives with infarction, unstable angina, and stroke. Protein C derivative human compared to wild-type activated human in acid substitutions result in increased resistance to main acid substitutions result in increased resistance to protein C. They also have longer half-lives in human blood and hence protein c. They also have longer half-lives in human blood and hence tenture either less frequent administration and/or smaller dosage than wild type human protein C for treating disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein C derivatives, useful for treating vascular occlusive disorder, hypercoagulable state, thrombotic disorder and disease states predisposing thrombosis, comprises specific amino acid substitutions -
                                                                                                             1141 GGTGAGGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCGGCTACCTC 1200
1081 GGGGGGCCCATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGACTGG 1140
                                                                                                                                        403 GlyGlyProMetValAlaSerPheHisGlyThrTrpPheLeuValGlyLeuValSerTrp 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein C; human; vascular occlusive; burn; transplantation; deep vein thrombosis; sickle cell; thalassemia; thrombotic disorders; myocardial infarction; angina; stroke.
                                                                                                                                                                                                                                    1201 GACTGGATCCATGGGCACATCAGAGACAAGGAAGCCCCCAGAAG 1245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 44-46; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36895 standard; Protein; 461 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein C derivative 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-APR-2000; 2000WO-US08722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0131801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-007227/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 461 AA;
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC83312.
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121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
                                                                                                            1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCGTGGAGGGGGAGGGGATGCATAGAGGAG 60
                                                                              181 AGCCTGTGCTGCGGCACGGCACGTGCATCGGCATCGGCAGCTTCAGCTGCGACTGC 240
                                                                                                                                                                         123 ArgSerGlyTrpGluGlyArgPheCysGlnArgGluValSerPheLeuAsnCysSerLeu 142
                                                                                                                                                                  241 CGCAGCGGGTGGGAGGGCCGCTTCTGCCAGCGGGAGGTGAGCTTCCTCAATTGCTCGCTG 300
                                                                                                                                                                                                         301 GACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGCTGTAGCTGT 360
                                                                                                                                                                                                                              361 GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT 420
                                                                                                                                                                                                                                        421 IGTGGGAGGCCCTGGAAGCGGATGGAGAAGCGCAGTCACCTGAAACGAGACACAGAA 480
                                                                                                                                                                                                                                                                                            481 GACCAAGAAGACCAAGTAGATCGGCGGCTCATTGATGGGAAGATGACCAGGCGGGGAGAC 540
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1021 GAGAACATGCTGTGTGCGGGCATCCTCGGGGACGGGAGGATGCCTGCGAGGGCGACACT 1080
                                        1081 GGGGGGCCCATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGG 1140
                                                                                  1141 GGTGAGGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTC 1200
          Human; Protein C; N-glycosylation; APC; activated protein C; precursor; serum half-life; chromosome 2q13-q14; stroke; mycoardial infarction; after venous thrombosis; disseminated intravascular coaqulation; DIC; sepsis; septic shock; embolism; pulmonary embolism; burn; pregnancy; bone marrow transplantation; major surgery; trauma; ARDS; coaqulant; adult respiratory distress syndrome; alpha-l antitrypsin.
                                                    Novel conjugate useful for treating or preventing septic shock, stroke and myocardial infarction, comprises non-polypeptide group covalently attached to protein C polypeptide comprising an attachment group -
                                                                                                                           1201 GACTGGATCCATGGGCACATCAGAGAAAGAAGGCCCCCAGAAG 1245
                                                                                                                                        /label= Activation_peptide 200..461
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Lys_Arg_dipeptide
                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Mature_protein_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pedersen AH, Freskgaard PO;
                                                                                                                                                                                                                                                                                                                                                                                                'label= Signal_peptide
                                                                                                                                                                                         AAU99001 standard; Protein; 461 AA.
                                                                                                                                                                                                                                                      Human Protein C precursor protein.
                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 76-77; 92pp; English.
                                                                                                                                                                                                                                 23-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MAXY-) MAXYGEN APS.
(MAXX-) MAXYGEN HOLDINGS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-2001; 2001WO-DK00679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-2000; 2000DK-0001560.
18-OCT-2000; 2000US-242268P.
21-JUN-2001; 2001DK-0000970.
21-JUN-2001; 2001US-300154P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-2002.
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The invention relates to a conjugate (I) comprising at least one non-conjugated more polypeptide comprising an anino acid sequence which differs a protein C polypeptide comprising an anino acid sequence which differs comprising an anino acid sequence which differs comprising a manno acid sequence which differs comprising a compression of the non-polypeptide group (e.g. an N-glycosylation cataciment group for the non-polypeptide group (iII) comprising a tataciment group for the non-polypeptide group (iII) comprising a cataciment group for the non-polypeptide group (iII) comprising a cataciment group exposed to the surface, with the proviso that substitution in a position (P) where (P) is an anino acid with a cataciment is not Thi235sr/Ala/His/LyGn/Gnl or Pho316ser/Ala/Thr/His/LygArg/Ash/Asp/Gul/Gly/Gnl or Pho316ser/Ala/Thr/ClyGnl or Pho316ser/Ala/Thr/His/LygArg/Ash/Asp/Gul, (2) an not-cotide sequence (V) encoding cyt/302ser/Ala/Thr/His/LygArg/Ash/Asp/Gul, (2) an not-cotide sequence (V) encoding cyt/302ser/Ala/Thr/His/LygArg/Ash/Asp/Gul, (4) a host coll (VII) (3) an expression vector (VI) comprising (V) (4) a host coll (VII) (3) an expression vector (VI) comprising (VI) (4) a host coll (VII) (3) an expression vector (VI) comprising (VI) the functional in vivo half-life or the serum half-life of a parent protein c polypeptide.

Comprising (V) or (VII); (5) increasing (VI) the functional in vivo half-life or the serum half-life, increased intravascular coagulation (DIC), sepsis, septic transplantation burns, pregnancy, major sugery/trauma or adult transplantation burns, pregnancy, major sugery/traum or adult transplantation burns, pregnancy, major sugery/traum or adult transplantation burns, pregnancy, major sugery/traum or adult transplantation or burns, pregnancy, major sugery/traum or adult transplantation or less prednancy major sugery/traum or adult transplantation or less prednancy major sugery/traum or distract conjugates have an increased sector. reduced immunogenicity and volument of destroad immunogenicit
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461 AA; Sequence

4415 0 0 0 0 0
Length: Matches: Conservative: Mismatches: Indels: Gaps:
1,37e-159 2298.00 100.00% 100.00% 98.33%
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Ouery Match:

US-09-763-153-1 (1-1245) x AAU99001 (1-461)

-60-SD	763-	US-09-763-153-1 (1-1249) A MINOR OF THE PROPERTY OF THE PROPER
δλ	н !	1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCGCGGGGGGGG
_	43	
~	61	ATCTGTGACTTCGAGGAGGCCAAGGAATTTTCCTTTTTTTT
qq	63	IlecysAspPheGluGluAlaLysGluLleFilecimon.
Οÿ	121	121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGAACACCACCACGACGAACAACAAAAAAAA
Db	83	TrpSerLysHisValAspGlyAspGlnCysLeuvalLcurrccanngc 240
QY	181	181 AGCCTGTGCTGCGGGCACGCACGTGCATCGACGCATCGGCAGCTTCHCLTCHCLTCACCCCCCCCCCCCCCCCCCCCCCCCC
QQ	103	
QY	24]	241 CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGGGGGGGGGG
ď	123	ArgSerGlyTrpGluGlyArgPheCysGlnArgGluValSerFneLeunSucfScar
3 8	301	GACAACGGCGGCTGCACCACATTACTGCCTAGAGGAGGTGGGCTGGCGGCGCTGTAGCTGT
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qq	143	3 AspasnGlyGlyCysThrHislyLysbccc

1141 GGTGAGGGCTGTGGGGCTCCTTCACAACTACGGCGTTTACACGAAAGTCAGCGGCTACCTC 1200 1021 GAGAACATGCTGTGTGTGGGGCATCCTCGGGGACGGGATGCCTGCGAGGACGCGACAGT 1080 1081 GGGGGGCCCATGGTGGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGACTGG 1140 961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCT 1020 363 IleLys1leProValValProHisAsnGluCysSerGluValMetSerAsnMetValSer 382 901 GGCTACCACAGCAGCCGAGAGAAGGAGGCCAAGAAACGGGACCTTCGTCCTCAACTTC 960 841 AGCGGCCTTGCAGAGCGCGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGG 900 781 CTGCACCTGGCCCAGCCACCTCTCGCAGACCATAGTGCCCATCTGCCTCCCGGAC 840 721 AAGGAGGTCTTCGTCCACCCAACTACAGCAAGAGCACCACGGACAATGACATCGCACTG 780 661 GTCAGGCTTGGAGAGTATGACCTGCGCGCGCTGGGAGAGTGGGAGCTGGACCTGGACATC 720 541 AGCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGCTGGCCTGCGGGGCCAGTGCTC 600 203 AspGlnGluAspGlnValAspProArgLeulleAspGlyLysMetThrArgArgGlyAsp 222 481 GACCAAGAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGGGGAGAC 540 421 TGTGGGAGGCCCTGGAAQCGGATGGAGAAGCGCAGTCACCTGAAACGAGACACAGAA 480 361 GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT 420 601 ATCCACCCTCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTT 1201 GACTGGATCCATGGGCACATCAGAGACAAGGAAGCCCCCAGAAG 1245 search completed: March 17, 2003, 17:31:03 Job time g δý q q QY δŏ 원 ò άý g g δλ g QY δŽ g g δλ οy g δŏ

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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using frame\_plus\_n2p model OM nucleic - protein search,

March 17, 2003, 17:26:59; Search time 51 Seconds (without alignments) 4693.622 Million cell updates/sec Run on:

BLOSUM62 ring table:

US-09-763-153-1 2337

Perfect score:

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1 gccaactccttcctggagga......acaaggaagcccccagaag 1245

0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries

Command line parameters:

MODEL-frame+\_n2p.model -DEV=xlp -Q=/Cgn2\_1/USPTO\_spool/US09763153/runat\_11032003\_084248\_2005/app\_query.fasta\_1.1415 -D=-PIR\_73 -QFMT=fastan -SUPETX=n2p.rpr -MINMATCH=0.1 -LOOPECH=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=60 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=20 -MODE=LOCAL -OUTPMT=ptc -NORM=ext -HARPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -USER=US09763153\_gCGR1\_1\_138\_erunat\_11032003\_084248\_2005 -NCPP=6 -ICPU=3 -NO\_XLPXY -NO\_MARP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_IIMEOUT=120 -WARN\_IIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

PIR\_73:\*

pir2:\* pir3:\* pir4:\* pir1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	protein C (activat	protein C (activat	protein C (activat	protein C (activat	Coadulation factor	coadulation factor	coagniation factor	coadulation factor	coaguiation factor					
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	Query Match Length DB	461	456	461	461	482	492	475	488	466	407	443	452	461	459
æ	Query	98.3	71.0	9.02	70.1	35.0	34.6	34.3	34.3	33.5	33.4	32.9	32.6	31.5	31.1
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11111111111111111111111111111111111111	55 55 57 59 60

## ALIGNMENTS

RESULT 1

protein C (activated) (EC 3.4.21.69) precursor - human M.Alternate names: autoprothrombin IIA; plasma protein C C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 16-Jul-1999 C;Accession: A22331; A25426; A21781; A23789; A00927 R;Foster D.C.; Yoshitake, S.; Davie, E.W. Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985 A;Reference number: A22331; MUID:85270390; PMID:2991887

A; Accession: A22331

A; Molecule type: DNA A; Residues: 1-461 <FOS1>

A)Cross-references: GB.M11228; NID:g190333; PIDN:AAA60166.1; PID:g190334
R; Plutzky, J; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
A; Title: Evolution and organization of the human protein C gene.
A; Reference number: A25426; MUID:86120978; PMID:3511471
A; Accession: A25426

A; Molecule type: DNA

A; Residues: 1.445,'L', 446-461 <PLU> A; Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332

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360 162 420 202 540 222 009 242 099 262 720 282 780 302 840 322 900

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961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTTT 1020
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                                                          181 AGCCTGTGCTGCGGGGACGCACGTGCATCGACGCATCGGCAGCTTCAGCTGCGACTGC 240
                                                                                                                                                                                                                       TGTGGGAGGCCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGACACAGAA 480
63 IleCysAspPheGluGluAlaLysGluIlePheGlnAsnValAspAspThrLeuAlaPhe 82
                                                                                                                                                                                                                                                                                                             CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 IleHisProSertrpValLeuThrAlaAlaHisCysMetAspGluSerLysLysLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 ValArgLeuGlyGluTyrAspLeuArgArgTrpGluLysTrpGluLeuAspLeuAspIle
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A Contents: annotation; beta-hydroxysaparic acid
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteins c also f
C;Comment: Protein C is synthesized in the liver as a single chain protein C also f
C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is c cidentics:
C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is c cidentics:
C;Comment: Protein C is synthesized in the amino end of the heavy chain; this reaction, C;Genetics:
A;Gene GBB: RRC
A;Cross-references: GDB:120317; OMIM:176860
A;Map position: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
A;Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 26/1; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 26/2; 
                                                                                                                                                                                                                                                                                                                                                                                                               A Molecule type: mRNA
A Molecule type: mRNA
A Pesidues: 1-64 (-8EC)
A Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120
B M. Milerich, J.P.; Broze Jr., G.J.
B Broze T. (55, 11397-11404), 1990
A Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation m A; Reference number: A44605; MUID:90293094; PMID:1694179
Contents: annotation; carbohydrate binding sites; activation peptide protein c arbohydrate binding sites; activation peptide protein C is glycosylated at Asn-329, and the beta form is not bills, R.J.; Ling, V.T.; Spellman, M.W.
Biol. Chem. 257, 510-25107, 1992
A; Title: O-linked fucose is present in the first epidermal growth factor domain of factor. A; Reference number: A44606; MUID:92184750; PMID:1544894
                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 'Q', 107-461 er0S2>
A; Residues: 'Q', 107-461 er0S2>
A; Residues: 'Q', 107-461 er0S2>
A; Crostences: GB: KO2059; NID: g190322; PIDN: AAA60164.1; PID: g190323
B; Beckmang, R.J.; Schmidt, R.J.; Santerre, R.F.; Plutzky, J.; Crabtree, G.R.; Long, G.L. Nucleic Acids Res. 13, 5233-5247, 1985
Nucleic Acids Res. 13, 5233-5247, 1985
A; Title: The structure and evolution of a 461 amino acid human protein C precursor and 1 A; Reference number: A23789; MUID: 85269639; PMID: 2991859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137Modified site: erythro-beta hydroxyaspartic acid (Asp) #status experimental 39,290,355/Binding site: carbohydrate (Asn) (covalent) #status experimental 1-212/Cleavage site: Arg-Leu (thrombin) #status experimental
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371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Foster, D.; Davie, E.W.
Proc. NaPl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
A;Title: Characterization of a cDNA coding for human protein C.
A; Réference number: A21781; MUID:84272714; PMID:6589623
A; Accession: A21781
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C; Comment: The agamma-carboxyglutamic acid residues arise by a posttranslational, withmin cognition of the thrombin-thrombomodulin cand residues arise by a posttranslational, witamin C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology C; Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding F; 129-00main: signal sequence (fragment) #status predicted <SIG> F; 30-39,Domain: gla domain homology <GLA> F; 30-39,Domain: propeptide #status predicted <PRO> F; 30-39,Domain: EGF homology <EGLA> F; 313-172,Domain: EGF homology <EGLA> F; 313-172,Domain: EGF homology <EGLA> F; 313-172,Domain: acit virtuation peptide #status experimental <ACH> F; 313-172,Domain: acit virtuation peptide #status experimental <ARP> F; 313-144,Domain: acit virtuation peptide #status experimental <ARP> F; 313-144,Domain: acit virtuation peptide #status experimental <AGPS F; 313-144,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #status F; 1169-128,137-148,144-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #status F; 136,289,350,Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 366/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A. Residues: 1-456 CLON-
B. Fernlund, P.; Stenflo, J.
J. Biol. Chem. 257, 12170-12179, 1982
A. Firtle: Annio acid Sequence of the light chain of bovine protein C.
A. Firtle: Annio acid Sequence of the light chain of bovine protein C.
A. Reference number: A18385, MUID:83007325; PMID:6896876
A. Molecule type: protein
A. Reference number: A18385
A. Molecule type: protein
A. Residues: 40-194 CERA
A. Molecule type: protein
A. Residues: 40-194 CERA
A. Molecule type: protein
A. Reference number: A18316; MUID:83105765; PMID:695087
A. Firtle: Annio acid Sequence of the heavy chain of bovine protein C.
A. Firtle: Annio acid Sequence of the heavy chain of bovine protein C.
A. Reference number: A18386; MUID:83007326; PMID:6896877
A. Reference number: A374; L280-12190, 1982
A. Firtle: Protein Type: protein
A. Reference number: A374; PW. CSTE>
A. Firtle: Protein Type: protein
A. Reference number: A374; PW. CSTE>
A. Firtle: Protein Type: protein
A. Reference number: A374; PW. CSTE>
A. Firtle: Protein Type: protein
A. Reference number: A374; PW. MUID:83131513; PMID:6304092
A. Firtle: Anniotation; activation: calcium binding
A. Contents: annotation; activation: calcium binding
A. Contents: annotation; activation: calcium binding
A. Contents: annotation; activation: calcium binding
A. Ference number: A374; PW. MUID:8313134; PMID:63060503
A. Title: Structural changes required for activation of protein C are induced by Ca2+ bin Reference number: A374; PMID:8313134; PMID:63060503
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                                                                                                                                                                                                       Protein C (activated) (EC 3.4.21.69) precursor - bovine (fragment)
N;Alternate names: autoprothrombin IIA; plasma protein C
C;Species: Bos primingenius taurus (cattle)
C;Date: 30-Nov-1980 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C;Accession: A26250; A18385; A18386; A00928
R;Long, G.L.; Balagaje, R.M.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5635-5656, 1984
Title: Cloning and sequence of liver cDNA coding for bovine protein C.
Reference number: A26250; MUID:885014826; PMID:6091100
1201 GACTGGATCCATGGGCACATCAGAGACAAGGAAGCCCCCCAGAAG 1245
                                      443 ASPTrpIleHisGlyHisIleArgAspLysGluAlaProGlnLys 457
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181 AGCCTGTGCTGCGGGCACGCCACGTGCATCGACGCATCGGCAGCTTCAGCTGCGACTGC 240
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              1.08e-95
1660.00
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71.81%
71.03%
                                                                               Best Local Similarity:
                                                          Percent Similarity:
Aliqnment Scores:
                                                                                                  Query Match:
                    Pred. No.:
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955 AACTTCATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATG 1014
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    42 AlaAsnSerPheLeuGluGluValArgAlaGlySerLeuGluArgGluCysMetGluGlu 61
                                                                     61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGGATGACACACTGGCCTTC
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-461 cOKA>
A; Cocossion: $18994
A; Cross references: EmBL; X6436; NID:956962; PIDN:CAA45617.1; PID:956963
A; Cross references: EmBL; X6436; NID:956962; PIDN:CAA45617.1; PID:956963
A; Attle: The CORA cloning and mRNA expression of rat protein C.
A; Reference number: $24312; MUID:92329550; PMID:1627650
A; Recession: $24312
A; Reference number: $24312; MUID:92329550; PMID:1627650
A; Reference number: $24312; MUID:92329560; PMID:1627650
A; Residues: 1-461 < COKA2>
A; Residues: Graph comparing a predicted company company as a predicted company a predicted company company a predicted company company
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C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Oct-1999
C; Accession: S18994; S2431
R; Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Submitted to the Embi. Data Library, February 1992
A; Description: The CDNA cloninig and mRNA expression of rat protein C.
A; Reference number: S18994
                                             955 AACTICATCAAGATICCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATG 1014
                                                                                                                                         1015 GTGTCTGAGAACATGCTGTGTGCGGCCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGC 1074
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coagulation factor Xa (EC 3.4.21.6) precursor - rat
C;Species: Rattus norvegitus (Norway rat)
C;Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 08-Dec-2000
C;Accession: S49075; JC4670; PS0191; PS0190; I62745
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                                                                                  GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCCGCAGTGAAGTTCCCT
                                                                                                                                                                                                                                                                                                              GACCAAGAAGACCAAGTA-----GATCCGCGGCTCATTGATGGGAAGATGACCAGGGGG
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A; Experimental source: 11ver
C; Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
C; Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
S;
C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F; 1-37/Domain: signal sequence #status predicted <PRO>
F; 34-41/Domain: Bad domain homology <GLA>
F; 34-41/Domain: propeptide #status predicted <PRO>
F; 34-196/Domain: Dropeptide #status predicted <PRO>
F; 31-196/Domain: EGF homology <EGS>
F; 31-190/Domain: EGF homology <EGS>
F; 31-1130/Domain: EGF homology <EGS>
F; 31-114/Domain: EGF homology <EGS>
F; 31-144/Domain: Activation peptide #status predicted <PCI>F; 31-445/Domain: activation peptide #status predicted <ACT>
F; 31-445/Domain: trypsin homology <TRY>
F; 31-445/Domain: trypsin homology <TRY>
F; 31-445/Domain: trypsin homology <TRY>
F; 31-31-30, 339-130, 146-159, 161-174, 182-319, 238-254, 373-387, 398-426/Disulfide bonds: #status F; 212-130, 339-150, 146-159, 161-174, 182-319, 238-254, 373-387, 398-426/Disulfide bonds: #status F; 212-309, 355/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 213-130, 339-355/Binding site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
Tsujimura, 111, 4914495, 1992
Tsize: Isolation and characterization of a mouse protein C cDNA.
A;Reference number: JX0210; MUID:92316897; PMID:1618739
                 1135 AGCTGGGGTGAGGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGC 1194
                                      61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AGCCTGTGCTGCGGGCACGGCACGTGCATCGACGGCATCGGCAGCTTCAGCTGCGACTGC
                                                                                                 1195 TACCTCGACTGGATCCATGGGCACATCAGAGACAAGGAAGCCCCCCAGAAG 1245
                                                                                                                         461
289
57
63
3
                                                                                                                                                                                                                        protein C (activated) (EC 3.4.21.69) precursor - mouse N.Alternate names: vitamin K-dependent serine proteinase
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Conservative:
Mismatches:
Indels:
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1637.50
83.98%
70.15%
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A; Residues: 1-461 <TAD>
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Best Local Similarity:
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Thromb. Res. 80, 63-73, 1995
A;Title: Evidence for competition between vitamin K-dependent clotting factors for intra A;Reference number: A58498; MUID:96093366; PMID:8578539
A;Accession: S49075
A;Accession: S49075
A;Residues: 1-482 AsrAl>
A;Residues: 1-782 AsrAl>
A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
A;Note: submitted to the EMBL: Data Library, June 1994
A;Note: neither the complete nucleic acid sequence nor the complete translation are show R;Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A;Title: Procession and expression of rat and human clotting factor-X-encoding cDNAs.
A;Reference number: JC4670; MUID:96194815; PMID:8647460
A;Molecule type: mRNA
A;Residues: 1-482 AsrA2>
A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
A;Molecule type: mRNA
A;Residues: 1-482 AsrA2>
A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
A;Molecule type: mRNA
A;Residues: 1-482 AsrA2>
A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
A;Molecule type: mRNA
A;Residues: 1-482 AsrA2>
A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
A;Molecule type: mRNA
A;Reference number: PS0190; MUID:92041742; PMID:1718949
Accession: PS0191
A;Cross-references number: PS0190; MUID:92041742; PMID:1718949
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165
79
153
49
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 41-58, 'X', 60-65 <ENJ1>
A; Accession: PS0190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.17e-43
818.50
54.71%
37.00%
35.02%
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Best Local Similarity:
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GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCCTGGAGCGGGGAGTGCATAGAGGAG 60

US-09-763-153-1 (1-1245) x EXRT (1-482)

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982 CACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTTCTGAGAACATGCTGTGTGCGGGC 1041
                                                                                                                                                                                                                                    121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
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                                                                                                  113 ThrGluGlyPheGluGlyLysAsnCysGluLeuPheValArgLysLeu---CysSerLeu 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 AspAsnGlyAspCysAspGlnPheCysArgGluGluGlnAsnSerValValCysSerCys 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 CysGlyLysThrAsnLysGlyArgAlaLysArgSerValAlaLeuAsnThrSerAsnSer 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 GlubroAspProGluAspLeuMetProAspAlaAspIleLeuTyrProThrGluSerPro 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            625 GCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTTGTCAGGCTTGGAGAGTATGACCTG 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332 PheArgGluAsnValAlaProAlaCysLeuProGlnLysAspTrpAlaGluAlaThrLeu 351
301 GACAACGGCGCCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGCTGTAGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           508 CTCATTGATGGGAAGATGACCAGGCGGGGAGACAGCCCCTGGCAGGTGGTCCTGCTG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACAGCAAGAGCACCACCGACAATGACATCGCACTGCTGCTGGACCTGGCCCAGCCCGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerGluLeuLeuAsnLeuAsnLysThrGluProGluAlaAsnSerAspAspValIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         565 GACTCAAAGAAGAAGCTGGCCTGCGGGGCAGTGCTCATCCACCCTCCTGGGTGCTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 AspGluGluThrAspGlyPheCysGlyGlyThrIleLeuAsnGluPheTyrIleLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 685 CGGCGCTGGGAGAAGTGGGAGCTGGACCTGGACATCAAGGAGGTCTTCGTCCACCCCAAC
                                                                                                                                                                                                                                                                                                                                                                             181 AGCCTGTGCTGCGGGCACGGCACGTGCATCGACGGCATCGGCAGCTTCAGCTGCGACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               466 AAACGAGACACAGAAGACCAAGAAGACCAAGTAGAT--------
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R;Fujikawa, K.; Titani, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A;Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha A;Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha A;Contents: annotation; activation
R:Sugo, T.; Blork, I.; Holmgren, A.; Stenflo, J.
Biol. Chem. 259, 5705-5710, 1984
A;Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxygluta A;Contents: annotation; calcium binding
R;Morita, T.; Jackson, C.M.
J. Biol. Chem. 261, 4008-4014, 1986
A;Reference number: A38025; MUD:8610210; PMID:3949800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with s C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vita C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Wene position: 13934

A; Description: atalyzes the proteolytic activation of prothrombin to thrombin in the A; Peathway: blood coagulation
C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol C; Superfamily: signal sequence *status predicted <SIG>
C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homol F; 1-15/Domain: signal sequence *status predicted <SIG>
F; 16-40/Domain: gland momilogy <GILA>
F; 18-180/Product: coagulation factor X light chain *status experimental <LCH>
F; 18-14/Domain: EGF homology <EGI>
F; 183-42/Product: coagulation factor X heavy chain *status experimental <HCH>
F; 183-42/Product: coagulation factor X heavy chain *status experimental <HCH>
F; 184-47, 54, 56, 59, 60, 65, 66, 69, 72, 75, 79/Modified site: gamma-carboxyglutamic acid (Glu) F; 75, 76, 90-101, 12-111, 12-111, 12-114, 13-14, 13-14, 13-14, 12-14, 12-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 13-14, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Contents: annotation; sulfate binding C.Comment: Factor Xa converts prothrombin to thrombin during blood clotting. C.Comment: The two chains are formed from a single-chain precursor by the excision of C.Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCTGGAGCGGGAGTGCATAGAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;275,321,418/Active site: His, Asp, Ser #status predicted
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                   A; Contents: annotation; active site
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52.27%
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Best Local Similarity:
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N.Alternate names: Stuart factor
C;Secies: Bos primigenius taurus (cattle)
C;Decies: Bos primigenius taurus (cattle)
C;Decies: Bos primigenius taurus (cattle)
C;Decies: 24-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C;Decies: 24-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C;Decies: 24-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
R;Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A;Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a A;Reference number: A22867; MUID:84247315; FMID:6336671
A;Molecule type: mRNA
A;Residues: 1-487 FCHNA
A;Residues: 1-487 FCHNA
A;Residues: 1-487 FCHNA
A;Reference number: A14997; MUID:80130563; FMID:6766735
A;Molecule type: protein
A;Reference number: A14997; MUID:80130563; FMID:6766735
A;Molecule type: protein
A;Residues: 41-102, N',104-180 CENF>
A;Molecule type: protein
A;Residues: A1-102, N',104-180 CENF>
A;Molecule type: protein
A;Reference number: A1-102, N',104-180 CENF>
A;Molecule type: protein
A;Reference number: A1-102, N',104-180 CENF>
A;Molecule type: protein
A;Reference number: A1-102, M',104-180 CENF>
A;Molec
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R; Titani, K.; Hermodson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D
Biochemistry 11, 4899-4903, 192.
A; Title: Bovine factor X.1a (activated Stuart factor). Evidence of homology with mammali
A; Reference number: Al2453; MUID:73053314; PMID:4264286
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A:Residues: 183-292,294-295, 'GDE', 299-334,336-348, 'AE', 351-354,356-441, 'GKFG', 446-492 <I
A:Residues: arbohydrate binding sites and disulfide bonds were determined
A:Note: carbohydrate binding sites and disulfide bonds were determined
B:Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
J. Biol. Chem. 264, 16897-16904, 1989
A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
A:Reference number: A34412; MUID:89380326; PMID:2789221
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                                                                                       1042 ATCCTCGGGGACCGGCAGGATGCCTGCGAGGGCGACAGTGGGGGGCCCCATGGTCGCCTCC 1101
                                                                                                                                                                                                                                                                            1102 TICCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGGGGTGAGGGCTGTGGGCTCCTT 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1162 CACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATCCATGGGCACATC 1221
                                                                                                                                                                                                                                                                                                                        445 GlyLysTyrGlylleTyrThrLysValThralaPheLeuLysTrpIleAspArgSerMet 464
385 ArgAsnThrCysArgLeuSerThrSerPheSerIleThrGlnAsnMetPheCysAlaGly 404
                                                                                                                                                       405 TyrAspAlaLysGlnGluAspAlaCysGlnGlyAspSerGlyGlyProHisValThrArg
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A; Residues: 183-196;199-209;216-233 <INO>
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A;Residues: 85-126 <PER>
A;Note: beta-hydroxyaspartic acid site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218, 153-163, 1993
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Eur. J. Biochem. 218,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: A12030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A34412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S39414
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Ωp	97	AsnGlnGlyHisCysLysAspGlyIleGlyAspTyrThrCysThrCys	112
δy	241	CGCAGCGGCTGGGAGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAAT	291
Dp	113		128
δλ	292	TGCTCGCTGGACAAACGCCGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGC	351
QQ	129		148
70 4	352	TGTAGCTGTGCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTG	411
3 8	41.7		4 50
ž 8	169	ArgPheProCysGlyLysPheThrGlnGlyArgSerArgArgTrpAlalleHisThrSer	188
Qγ	469		504
9	189	GludspalaLeudspalaSerGluLeuGluHisTyrAspProdlaAspLeuSerProThr	208
	504		504
q	209	${\tt GluSerSerLeuAspLeuLeuGlyLeuAsnArgThrGluProSerAlaGlyGluAspGly}$	228
ΟŽ	505		50
qq	229		248
δŏ	553	GTGGTCCTGCTGGACTCAAAGAAGCTGGGGGCGGGGGCAGTGCTCATCCACCCTCC	612
o O	249		268
οy	613	TGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTTGTCAGGGTTGGA	672
Ωp	269		288
کې ځ	673	GAGTATGACCTGGGGCGCTGGGAAAGTGGGAGCTGGACCTGGACATCAAGGGGGTCTTC :::::::::::::::::::::::::::::	732
łä			o (o
<u>ک</u> ۾	309	GTCCACCCCAACTACAGACAGGACCCACCGACAATGACATGGCACTGCTGCCC	792 328
ò	793		852
g q	329	ThrProlleArgPheArgArgAsnValAlaProAlaCySLeuProGluLySAspTrpAla	4
οy	853		606
	349		364
අධ	910	AGCAGCCGAGAGAGAGAGAAACCGCACCTTCGTCCTCAACTTCATCAAGATT           ::::::::::::::::::::::::::	969 381
ċ	0.70		1038
S q	382		0.2
οy	1030		1089
QQ	402		421
Qy	1090	ATGGTCGCCTCCTTCCACGCACCTGGTTCCTGGTGGGCCTGGTGAGGTGAGGGC	1149 441
δ d	1150	TGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATC	1209
g	442		461

δλ	1210
qq	462 AspLysIleMetLysAlaArgAlaGlyAlaAlaGlySerArgGlyHisSer 478
oy G	1231 GAAGCCCCC 1239            479 GluAlaPro 481
RESULT EXCH COAGUL	factor Xa (EC 3.4.21.6) precursor
κίς Σ΄Ο΄ Σ΄Ο΄	N;Alternate names: Virus-activating proceinase C.Species: Gallus gallus (chicken) C:Date: 12-Feb-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C;A	C;Accession: S15838; S20380; S20381 R;Suzuki, H; Harada, A; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.;
A;T	Febs. Lett. 283, 281-283, 1931. A.Title: Primary structure of the virus activating protease from chick embryo. Its id A;Reference number: S15838; MUID:91257322; PMID:2044767
A S X A A A	A;Accession: S15838 A;Status: not compared with conceptual translation A;Wolecule type: mRNA
A A A	A;Residues: 1-475 <suz> A;Cross-references: DDBJ:D00844; NID:g222869; PIDN:BAA00724.1; PID:g222870 R:Gotch, B.: Yamauchi, F.; Odasawara, T.; Nagai, Y.</suz>
FEB A; T	S Lett. 296, 274-278, 1992 itle: Isolation of factor Xa from chick embryo as the amniotic endoprotease respon
A; B	: S20380; MUID:92164779; PMID:1537 )
A; W	A,Molecule type: protein A;Residues: 41-55 <go2></go2>
A;A	A; Moleosion: S20381 A; Moleole type: protein
C, F	
A;D	tion of prothrombin to thrombin i
Ω.Ω. Ω.Χ.	C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; C; Reywords: beta-hydroxyaspartto caid; blood coagulation; calcium binding; carboxyglu F:1-20 /nomain: eighal equipments predicted (STR)
F F F	1.4/Jonain: propertie #status predicted <pro> 5.84/Jonain: propertie #status predicted <pro></pro></pro>
H H	1-185/Product: coagulation factor X light chain #status experimental <lch> 0-121/Domain: EGF homology <eg1></eg1></lch>
F F F	29-167/Domain: EGF homology <eg2> 64-475/Product: coagulation factor X heavy chain #status predicted <hch> 86-34/Aromain: artivation nentide #status predicted <adt></adt></hch></eg2>
H H H	40-747/Poduct: coagulation feptine "status premiora" Ant. 4475/Product: coagulation factor Xa heavy chain #status experimental <ahc> 41-468/Anomain: trynsin homelogy <try></try></ahc>
FFFF 40110	46,47,54,56,59,60,65,66,69,72,73,79/Modified site: gamma-carboxyglutamic acid (Glu) 157-62,90-101,95-110,112-121,129-140,136-152,134-167,175-348,247-252,267-283,396-410 103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted 196,207,228,285/ABinding site: carbohydrate (Asn) (covalent) #status predicted 196,207,228,285/Active site: Msp, Ser #status predicted
Alignm Pred. Score: Percen Best L	ent Scores: 2.47e-42 No.: 801.50 t Similarity: 54.778 ocal Similarity: 36.148 Match: 34.308
DB:	1 Gaps:
-Sn	-09-763-153-1 (1-1245) x EXCH (1-475)
δŏ	GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCCTGGAGCGGGAGTGCATAGAGGAG
QQ	AlaAsnSerPheLeuGluGluMetLysGlnGlyAsnIleGluArgGluCysAsnGluGlu
ΟŊ	
qq	61 ArgCysSerLysGluGluAlaArgGluAlaPheGluAspAsnGluLysThrGluGluPhe 80

QY	121	TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGCCTTGGAGCACCCGTGCGCC 180    ::::::	
Qy Db	181 95		
Qy	241		
ò	301	GACAACGCGCTGCACGCATTACTGCCTACAGGAGGTGGGCTGGCGGCGC3	
	132		
S a	352 152	TGTAGCTGTGCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTG 411                     CysSerCysThrSerGlyTyrGluLeuAlaGluAspGlyLysGlnCysValSerLysVal 171	
οy	412	AAGTTCCCTTGTGGGAGGCCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGA	
qa a	172	LysTyrProCysGlyLysValLeuMetLysArgIleLysArgSerVallleLeuProThr 19	
g ć	192	GAC	
οy	486	48	
QQ	212	GluGluValPheThrThrThrGluSerProThrProProArgAsnGlySerSer 231	
οy	487	GAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGGGAGAC 540	
qq	232	:::	
ΟŊ	541	AGCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGCTGGCCTGCGGGGGGGG	
QQ	252	CysproTrpGlnAlaValLeu1leAsnGluLysGlyGluGluPheCysGlyGlyThr11e 271	
Qy Db	601	ATCCACCCCTCCTGGGTGCTGACAGCGCCCCACTGCATGAGTCCAAGAAGCTCCTT 660 :::::: LeuAsnGluAspPheIleLeuThralaAlaHisCysIleAsnGlnSerLysGluIleLys 291	
<b>&gt;</b>	661	7	
	292	ValValValGlyGluValAspArgGluLysGluGlüHisSerGlüThrThrHisThrAla 311	
Oy Dp	312	AAGGAGGTCTTCGTCCACCCCAACTACAGCAAGAACACCACCGACAATGACATCGCACTG 780	
λά	781		
. A	332		
λά	841	AGCGGCCTTGCAGAGCGCGAGCTCAATCAGGCGGCCAGGAGACCCTCGTGACGGGC 897	
Q ·	352	AlaAspPheAlaAsnGluValLeuMetAsnGlnLysSerGlyMetValSerGly 369	
λο O	370	TTCGTCCTCAAC	
y d	958 385	TTCATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTG 1017 ::::::::                 ::                :: ValLeuGluValProTyrValAspArgSerThrCysLysGlnSerThrAsnPheAlaIle 404	
λα		TCTGAGAACATGCTGTGGGGCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGCGAC 1077	
q	405	ThrGluAsnMetPheCysAlaGlyTyrGluThrGluGlnLysAspAlaCysGlnGlyAsp 424	

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276,322,419/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 183-234 <1NO>
A; Note: 1000 State of the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reference number: A49458; MUID: 93360277; PMID: 8355279
A; Contents: annotation; X-ray crystallography, 2.2 angstroms
C; Comment: The two chains held together by one disulfide bond are formed from a single-c
C; Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;57-62/Disulfide bonds: #status predicted
F;90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443,
F;90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443,
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
199,211/Binding site: carbohydrate (Asn) (covalent) #status experimental
21,231/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bla
A; Cross-references: GB:M33297; NID:g183860; PIDN:AAA52636.1; PID:g553330; Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Mol. Biol. 232, 947-966, 1993
Mol. Biol. 232, 947-966, 1993
Fille: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: translation not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 13q34-13q34
A; Introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
A; Note: deficiency of this factor causes Stuart disease
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:119890; OMIM:227600
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54.55%
35.25%
34.30%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA A; Residues: 1-23 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: I54051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
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970 cccgrggrccccccacaargagrgcagcgaggrcargagcaacarggrgrrcrgagaacarg 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             403 PheCysAlaGlyTyrAspThrLysGlnGluAspAlaCysGlnGlyAspSerGlyGlyPro 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 HisGluLysGlyArgGlnSerThrArg------LeuLysMetLeuGluVal 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 TOTGGGAGGCCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGACACAGAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 CysGlyLys-----GlnThrLeuGluArgArgLysArgSerValAlaGlnAlaThrSer 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 AsnAsnLeuThrArglleValGlyGlyGlnClySLysAspGlyGluCysProTrpGln 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 TyrileLeuThralaAlaHisCysLeuTyrGlnAlaLysArgPheLysValArgValGly 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              733 GICCACCCCAACIACAGCAAGAGCACCACCGACAAIGACAICGCACIGCIGCACCIGGCC 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           793 CAGCCCGCCACCTCGCAGACCATAGTGCCCATCTGCCTCCCGGACAGCGGCCTTGCA 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 ThrProlleThrPheArgMetAsnValAlaProAlaCysLeuProGluArgAspTrpAla 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaargGlyTyrThrLeuAlaaspAsnGlyLysAlaCysIleProThrGlyProTyrPro 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 ProThrGluAsnProPheAspLeuLeuAspPheAsnGlnThrGlnProGluArgGlyAsp 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 553 GIGGICCIGCIGGACICAAAGAAGAAGCIGGCCIGCGGGGCAGIGCICAICCACCCCCCC 612
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                                                                                                                                                                                                                                                 241 CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                 121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCCGTGCGCC 180
61 ThrCysSerTyrGluGluAlaArgGluValPheGluAspSerAspLysThrAsnGluPhe 80
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                                                                                                                                                81 TrpAsnLysTyrLysAspGlyAspGlnCysGluThrSerPro-
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                                                                                                                                                                                                                                                                                                                                                                                                        gulation factor VIIa (EC 3.4.21.21) precursor [validated] - human sapiens (man)
Decises: Homo sapiens (man)
CACCESS: Homo sapiens (man)
CACCESS: Homo A28322; A23819, A31186; B31186; S65524
FACCESS: P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murr Proc. Natl. Acad Sci. U.S.A. 84, 5158-5162, 1987
A; Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend A; Reference number: A28322; MUID:87260948; PMID:3037537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 213-466 < TH2>
A; Residues: 213-466 < TH2>
Bjoorn, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Peder Blol. Chem. 266, 11051-11057, 1991
Fille: Human plasma and recombinant factor VII. Characterization of O-glycosylations a Reference number: A40529; MUID:91220411; PMID:1904059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-466 <HAG>
A; Cross-references: GB:M13232; NID:g182799; PIDN:AAA88040.1; PID:g182801
R; Thim, L.; Broern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochemistry 27, 7785-7793, 1988
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Oagulation factor IX in the presence of calcium and tissue factor

Sylathway

C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; C; Reywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F; 11-20/Domain: signal sequence #status predicted <SIG>
F; 12-60/Domain: propeptide #status predicted <PRO>
F; 45-104/Domain: Gla domain homology <GLA>
F; 61-212/Product: coagulation factor VIIa light chain #status experimental <MAI>
F; 110-141/Domain: EGF homology <EGL>
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Bur. J. Blochen. 234, 293-300, 1995
A;TitLe: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox A; Reference number: 863524; MUID:96096752; PMID:8529655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Cross-references: GB:J02933; NID:g180333; PIDN:AAA51983.1; PID:g180334
R;Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart,
RCC. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A;Title: Characterization of a cDNA coding for human factor VII.
A;Reference number: A23819; MUID:86205965; PMID:3486420
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1090 ATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGGGGTGAGGGC 1149
                                                                                                                 1150 TGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCGGCTACCTCGACTGGATC 1209
                                    A;Map position: 13q34-13q34
A;Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C;Function:
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A; Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Contents: annotation; carbohydrate binding sites
                                                                                                                                                                                                                                      1210 CATGGGCACATCAGAGCACAAGGAAGCCCCCCAG 1242
                                                                                                                                                                                                                                                                                                463 AspArgSerMetLysThrArgGlyLeuProLys 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 61-212 <THI>
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F:151-187/Domain: EGF homology <EG2>
F;213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F;213-447/Domain: trypsin homology <TRY>
F;213-447/Domain: trypsin homology <TRY>
F;66,67.74,76,79,80,85,86,89,95/Modlfied site: gamma-carboxyglutamic acid (Glu) #stat F;77-82,110-121,115-130,132-141,151-162,158-172,174-187,195-322,219-224,238-254,370-3 F;112,120/Binding site: carbohydrate (Ser) (covalent) #status experimental F;205,382/Binding site: carbohydrate (Asn) (covalent) #status experimental F;205,382/Binding site: arbohydrate (Asn) (covalent) #status experimental F;212-213/Cleavage site: Arg-1le (coagulation factor XIIa) #status experimental F;215-33302,404/Active site: His, Asp, Ser #status predicted F;350-351/Cleavage site: Arg-1le (coagulation factor XIa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 GlnCysSerPheGluGluAlaArgGluIlePheLysAspAlaGluArgThrLysLeuPhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AGCCTGTGCTGCGGGCACGCCACGTGCATCGACGGCATCGGCAGCTTCAGCTGCGACTGC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 LeuProAlaPheGluGlyArgAsnCysGluThrHisLysAspAspGlnLeuIleCysVal 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 ArgCysHisGluGlyTyrSerLeuLeuAlaAspGlyValSerCysThrProThrValGlu 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::||||||||:::
193 TyrProCysGlyLys---IleProIleLeuGluLysArgAsnAla------ 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 CGCAGCGGCTGGGAGGGCCGCTTCTGCCAG---CGCGAGGTGAGCTTCCTCAATTGCTCG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 AGCTGTGCCCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCCAGTGAAG 414
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us-09-763-153-1.n2p.rpr

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US-09-763-153-1 (1-1245) x KFBO7 (1-407)
91-127/Domain: EGF homology <EG2>
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C; Function:

C; Superfamily:

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A; Residues: 58-62, /X', 64-68 < MCM>
A; Residues: 58-62, /X', 64-68 < MCM>
A; Note: the residue designated 'X' was determined to be hydroxyaspartic acid
B; Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,
J. Blochem. 104, 867-868, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1-407 < TAK>
R; McMullen, B.A.; Fujikawa, K.; Kisiel, W.
P; McMullen, B.A.; Fujikawa, K.; Kisiel, W.
P; Ochem. Biophys. Res. Commun. 115, 8-14, 1983
Pitle: The occurrence of beta hydroxyaspartic acid in the vitamin K-dependent blood pference number: A20274; MUID:83308813; PMID:6688526
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C;Species: Bos primigenius taurus (cattle)
C;Species: 12-May-1990 Headuence_revision 23-Mar-1995 #text_change 16-Jul-1999
C;Accession: A31979; C20274
R;Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, EJ Blol. Chen. 263, 14686-14877, 1988
A;Title: Bovine factor VII. Its purification and complete amino acid sequence.
A;Reference number: A31979; MUID:89008362; PMID:3049594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1111 ACCTGGTTCCTGGTGGCCTGGTGAGCTGGGGTGAGGCCTGTGGGGCTCCTTCACAACTAC 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1171 GGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATCCATGGGCACATCAGAGACAAG 1230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 ArgLysValGlyAspSerProAsnIleThrGluTyrMetPheCysAlaGlyTyrSerAsp 394
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                                          766 AATGACATCGCACTGCTGCACCTGGCCCAGCCCGCCACCTCTCGCAGACCATAGTGCCC 825
                                                                                                                                                                                                                                                                 321 LeuCysLeuProGluArgThrPheSerGluArgThrLeuAlaPheVal---ArgPheSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 AGCIGIGGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAG 414
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	335 AGLUGAGCCTGGGGGGACCTCCTGCGGGGACCTCCTGCAGTGCCCCCCGCAGTGAG 414 152 ArgCysHisGluGlyTyThkLeuLeuProAsnClyValSerCysThrProThrValasp 171 415 TTCCCTTGTGGGAGGCCTGGAAGCGGATGGAGAAGAGAGAG		260 GlnValArgHisValAlaGanGTCTTGGTCCACCAACTAAGCAAGCAACCAACGAAC 765 3::::::::::::::::::::::::::::::::::::	319 ArgvalserGlyTrpGlyGlnLeuLeuTyrArgGlyAlaLeuAlaArgGlu 335 937 AACGGCACCTTCGTCCTCAACTTCATCAAGATTCCGGTGGTCCGGCACATGAGTGCAGC 996 937 AACGGCACCTTCGTCAACTTCATCATCATCGTGGTCCGGCAATGAGTGCAGC 996 936	1042 ATCCTCGGGGACCGCAGGAFGCCTGCGAGGGCGACGGGGGCCCATGGTCGCCTCC 1101 371 TyrLeuAspG1ySerLysAspAlaCysLysG1yAspSerG1yG1yProHisAlaThrSer 390 1102 TTCCACGGCACTGGTTCCTGGTGGCCTGGTGGGGTGAGGGTGTGGGCTCTT 1161 :::            :::
	6 6 6 6	9 6 6 6	н	9 do	0 d d d d d d d d d d d d d d d d d d d
Oy 766 AATGACATGGCACTGGCCCAGCCCGCCACCCTCTGGCAGACCATAGTGCCC 825  1::   ::	1006 AGCAACATGGTGTCTGAGAACATGCTGTGGGGGCATCTCGGG 315 ArgGlnArgProGlyGlyProValValThrAspAsnMetPheCysAlaGlyTyrSerAsp 1051 GACCGGCAGGAGGCGAGGGGGGCCCATGGTCGCCTCCTTCCAGGC 335 GlySerLysAspAlaCysLysGlyAspSerGlyGlyProHisAlaThrArgPheArgGly 1111 ACCTGGTTCCTGGTGGGCTGGAGGGTGAGGGTGGGCTGTTCAAACTAC 1111 ACCTGGTTCCTGGTGGCCTGGTGGGGTGAGGGTGGGGTG	Qy 1171 GGCGTTACACCAAAGTCAGCCGCTACCTCGACTGGATCCATGGGCAC 1218	59, 231-238, 1993 lete nucleotide sequence of the cDNA encoding rabbit coagulation factor under: 146932; MUID:93190306; PMID:8383365 liminary; translated from GB/EMBL/DDBJ e: mRNA 443 < GB:556300; NID:9266294; PID:9266295 : coagulation factor X; EGF homology < GLA> in: EGF homology < EGLA> in: EGF homology < EGLA> in: EGF homology < EGLA> in: trypsin homology < TRX>	Alignment Scores:  Pred. No.: Scores: 769.50 Matches: Percent Similarity: Best Local Similarity: 73.72% Manatches: Recont Match: 32.93% Indels: DB: US-09-763-153-1 (1-1245) x 146932 (1-443)	Oy 1 GCCAACTCCTGGAGGAGCTCCGTCAGCAGCTGGAGCGGAGTGCATAGAGGAG 60

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1066 TGCGAGGGCGACAGTGGGGGCCCATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTG 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 946 TTCGTCCTCAACTTCATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATG 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1006 AGCAACATGGTGTCTGAGAACATGCTGTGTGCGGGCATCCTCGGGGACCGGCAGGATGCC 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1126 GGCCTGGTGAGCTGGGGTGAGGGCTGTGGGGCTTCACAACTACGGCGTTTACACCAAA 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 CysGlnGlyAspSerGlyGlyProHisValThrGluValGluGlyIleSerPheLeuThr 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       784 CACCTGGCCCAGCCGCCACCTCTCGCAGACCATAGTGCCCCATCTGCCTCCCGGACAGC 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :::||| ::::||| :::::|||:::||| 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 LysPheThrIleTyrAsnAsnMetPheCysAlaGlyPheHisGluGlyGlyLysAspSer 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               730 ITCGICCACCCCAACTACAGCAAGAGCACCACC----GACAATGACAICGCACIGCIG 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GCCGGCCAGGAGACC 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 Gln---valLeuLeuAsnGlyLysValAspAlaPheCysGlyGlySerIleIleAsnGlu 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             670 GGAGAGTATGACCTGCGGCGCTGGGAGAAGTGGGAGCTGGACCTGGACATCAAGGAGGTC 729
                                                                                                                                                                                                                                                                                                                                  192 ASNMetAspTyrGluAsnSerThrGluValGluLysIleLeuAspAsnValThrGlnPro 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 550 CAGGIGGICCIGCIGGACICAAAGAAGAAGCIGGCCIGCGGGCCAGIGCICAICCACCCC 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               610 TCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTTGTCAGGCTT 669
313 TGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGC------TGTAGCTGTGCG 363
                                           134 CysLysGlnPheCys-----LysLeuGlyProAspAsnLysValValCysSerCysThr 151
                                                                                                                    424 GGGAGG------CCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGAC 474
                                                                                                                                                                                                                                       172 GlyargValSerValPrOHisIleSerMetThrArgThrArgAlaGluThrLeuPheSer 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 GlyGluHisAsnThrGluLysArgGluHisThrGluGlnLysArgAsnValIleArgThr
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                                                                                                                                                                                                                                                                                                                                                                                                                      ---CCGCGGCTCATTGATGGAAGATGACCAGGCGGGGGAGACAGCCCCTGG
                                                                                              364 CCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coagulation factor IXa (BC 3.4.21.22) precursor [validated] - human N;Alternate names: antihemophilic factor B; Christmas factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         475 ACAGAAGACCAAGACCAAGTAGAT----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            844 GGCCTTGCAGAGCGCGAGCTCAATCAG------
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A. Residues: 1-452 < AXE
C. Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C; Reywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
C; Reywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
C; Reywords: beta-hydroxyaspartic acid; blood coagulation; captured extents predicted < RIG>
F; 12.7-40/Domain: EGF domain homology < GLA>
F; 24-84/Domain: EGF homology < REG>
F; 127-163/Domain: EGF homology < REG>
F; 127-163/Domain: EGF homology < REG>
F; 128-445/Domain: EGF homology < RGS>
F; 44, 55, 59, 60, 65, 66, 69, 72, 75, 79/Modfied site: gamma-carboxyglutamic acid (Glu) #s
F; 27-62, 90-101, 95-110, 112-121, 127-138, 134-148, 150-163, 171-326, 243-259, 373-387, 398-426/Di
F; 258, 306, 402/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GB:M21757; NID:g972719; PIDN:AAA75006.1; PID:g163948

Nelrod, J.H.; Read, M.S.; Brinkhous, K.M.; Verma, I.M.

DC. Natl. Acad. Sci. U.S.A. 87, 5173-5177, 1990

Title: Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophilic A;Reference number: I46201; MUID:90311364; PMID:2367529
                                                                                                                                                                                                 Coagulation factor IXa (EC 3.4.21.22) precursor - dog
C; Species: Canis lupus familiaris (dog)
C; Species: Canis lupus familiaris (dog)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: A30351; H.H.; Ware, J.L.; Stafford, D.W.; High, K.A.
Blood 74, 207-212, 1989
A; Title: Molecular cloning of a CDNA encoding canine factor IX.
A; Reference number: A30351; MUID:8932338; PMID:2752110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTCTGGTCCAAGCAC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCGACGGTGACCAGTGCTTGGTCTTGCACCACCCGTGCGCCCAGCCTGTGCTGC 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnAspGlyValCysLysAspAspIleAsnSerTyrGluCysTrpCysArgAlaGlyPhe 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTGGACAACGGCGGC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 GlyHisValGlyValTyrThrArgValSerArgAspThrGluTrpLeuSerArgLeuMet 429
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158
73
141
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Mismatches:
Indels:
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Matches:
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763.00
53.97%
36.92%
32.65%
                                                               1222 AGAGACAAG 1230
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A; Residues: 1-452 <EVA>
                                                                                                             430 ArgSerLys 432
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A; Note: 194-Thr was also found
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A. Residues: 30-92 < KOE>
R. Molecule type: DNA
A. Residues: 30-92 < KOE>
R. Molecule type: DNA
A. Residues: 30-92 < KOE>
R. Molecule type: DNA
A. Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat
A. Recession: A22673
A. Molecule type: mRNA
A. Recession: A22673
A. Molecule type: mRNA
A. Residues: 1-193, TY, 195-461 < ANG
A. Title: Isolation of a human anti-haemophilic factor IX CDNA clone using a unique 52-ba
A. Cross-reference unmber: A21337; MUID: 83220788; PMID: 6687940
A. Cross-references: GB: J00137; NID: 9182510; PIDN: AAA52763.1; PID: 9182611
B. Jagadeeswaran, P.: Lavelle, D.E.: Kaul, R.; Mohandas, T.; Warren, S.T.
A. Title: Isolation and characterization of human factor IX CDNA: identification of Taq I
A. Title: Isolation and characterization of human factor IX CDNA: identification of Taq I
A. Title: Isolation and characterization of human factor IX CDNA: identification of Taq I
A. Reference number: A37546; MUID: 84300526; PMID: 6089357
A. Molecule A. Molecul
C; Date: 17-Dec-1982 #sequence_revision 30-Jun-1987 #text_change 15-Sep-2000
C; Accession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A26
B; Coccession: A00922; A37570; A30511; A32989; A22673; A21337; A37546; A30623; A60486; A26
B; Coccession: A00922; A376-3750, 1985
A; Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B). A; Reference number: A00922; MUID:86000558; PMID:2994716
A; McCession: A00922
A; Molecule type: DNA
A; Residues: 1-461 <VOS>
A; Residues: 1-461 <VOS>
A; Cross-references: GB:XC2402; NID:9182612; PIDN:AAB59620.1; PID:9182613
B; Anson, D.S.; Choo, K.H.; Rees, D.J.G.; Giannelli, F.; Gould, K.; Huddheston, J.A.; BrG
A; Title: The gene structure of human anti-haemophilic factor IX.
A; Reference number: A37570; MUID:84236100; PMID:6329734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Cross-references: EMBL:X55008; NID:g311288; PIDN:CAB38245.2; PID:g4469253
R;Koeberl, D.D.; Bottema, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
M. J. Hum. Genet. 45, 448.457, 1989
A;Title: Functionally important regions of the factor IX gene have a low rate of polymor A;Reference number: A32989; MUID:89371752; PMID:2773937
A;Accession: A32989
A;Status: not compared with conceptual translation
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A.Rolecule type: MRNA
A.Title: Development of an immunoaffinity process for factor IX purification.
A.Reference number: A60486; MUID: 90194857; PMID: 2316207
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A; Title: The putative factor IX gene promoter in hemophilia B Leyden.
A; Reference number: A30511; MUID:88327116; PMID:3416069
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A; Residues; 38-193, Tr,195-326 <JAG>
A; Cross-references; GB:M35672
R; Kurachi, K.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
A; Rille: Isolation and characterization of a cDNA coding for human factor IX.
A; Reference number: A30623; MUID:83065193; PMID:6959130
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Residues: 1-461 <ANS>
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A; Molecule type: protein
A; Medidues: 47-52, Xx, 55-60, Xx, 65 < THA>
A; Residues: 47-52, Xx, 55-60, Xx, 18:siel, W.
B; McMullen, B.A.; Fujikawa, K.; Kisiel, W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A; Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood
A; Reference number: A20274; MUID:883308813; PMID:6688526
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A. Molecule type: proteins expressed in recombinant system
R. Jallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meulie
EMBO J. 9, 3295-3301, 1990
A. Title: Characterization of recombinant human Factor IX expressed in transgenic mice
A. Reference number: $12058; MUID: 91006024; PMID: 2209546
A. Accession: $12058
A. Molecule type: mRNA; protein
A. Residues: 1-68 < JAL.
A. Note: processed forms expressed in recombinant system
A. Note: processed forms expressed in recombinant system
A. Note: processed forms expressed in recombinant system
A. Molecule type: protein
A. Residues: $12377; MUID: 90151623; PMID: 2406129
A. Title: The first EGF-like domain from human factor IX contains a high-affinity calc
A. Accession: $12377; MUID: 90151623; PMID: 2406129
A. Molecule type: protein
A. Molecule type: protein
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A; Residues: 105-109, "X', 111-115 < MCM>
A; Residues: 105-109, "X', 111-115 < MCM>
Bur. J. Blochem. 172, 565-572, 1988
A; Title: Characterisation of two differently processed forms of human recombinant fac
A; Accession: S02527; MUID: 88166735; PMID: 3280312
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A. Residues: 'D', 204,'X', 206-211;212,'D', 214,'X',216-221,'D' <AGA>
A. Note: the residues designated 'X' were determined to be threonine bound to carbohyd A. Note: the residues designated 'X' were determined to be threonine bound to carbohyd C. Clin. Invest. 61, 1528-1538, 1978
A. Tille Activation of human factor IX (Christmas factor).
A. Reference number: A18483: MUID:78194509; PMID:659613
A. Contents: annotation; activation; act
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A; Residues: 290-359 <RE2>
A; Residues: 290-359 <RE2>
A; Residues: 290-359 <RE2>
B; Residues: 290-359 <RE2>
B; Reference GB: MI9063; NID: 9182622; PIDN: AAA52456.1; PID: 9182623
B; Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Biochamistry 33, 5167-5171, 1994
A; Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically A; Reference number: A54255; MUID: 94227047; PMID: 8172892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
J. Biol. Chem. 259, 5698-5704, 1984
A.Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-bind
A; Reference number: A37543; MUID:84185715; PMID:6425296
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A.Residues: 444-461 <RES>
A.Fesidues: 444-461 <RES>
A.Cross-reference BE:866752; NID:9439773; PIDN:AAB28588.1; PID:9439774
R.Stoflet, E.S.; Koeberl, D.D.; Sarkar, G.; Sommer, S.S.
Science 239, 491-494, 1988
A.Title: Genomic amplification with transcript sequencing.
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A; Status: translated from GB/EMBL/DDBJ
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C; Superfamily: coagulation intrinsic pathway
C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F; 1-20/Domain: signal sequence #status predicted 450075
F; 21-40/Domain: propeptide #status experimental <PPT>
F; 21-40/Domain: Gla domain homology <GGA>
F; 31-91/Domain: EGF homology <GGA>
F; 31-191/Product: coagulation factor IXa light chain #status experimental <ALC>
F; 31-10/Domain: EGF homology <EGC>
F; 31-10/Domain: EGF homology <EGC>
F; 31-10/Domain: activation peptide #status experimental <ACT>
F; 227-454/Domain: activation peptide #status experimental <ACT>
F; 227-454/Domain: trypsin homology <ERX>
F; 227-454/Domain: trypsin homology <ERX>
F; 237-454/Domain: trypsin homology <ERY>
F; 237-454/Domain: trypsin homology <ERX>
F; 237-454/Domain: trypsin homolog
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R; Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle
submitted to the Brookhaven Protein Data Bank, November 1991
A; Reference number: A51252; PDB:11XA
A; Contents: annotation; conformation by (1)H-NMR, residues 92-130
Note: recombinant form expressed in yeast
comment: Factor IX is activated by factor XIa, which excises the activation peptide pr
comment: The gamma-carboxyglutemic acid residues arise by posttranslational, vitamin K
comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stre
                                                                                                                                                                                                                                                                                                       A; Contents: annotation; signal sequence cleavage site
R; Suehiro, K.; Kawabata, S. I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,
J. Biol. Chem. 264, 21257-21265, 1989
A; Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptopha
A; Reference number: A30622; MUID: 90078229; PMID: 2592373
A; Contents: annotation; sequence of mutant B(M) Nagoya
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                                                                                                                                                          R;Bentley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G. Cell 45, 343-348, 1986
A;Title: Defective propeptide processing of blood clotting factor IX caused by mutation A;Reference number: A37545; MUID:86189947; PMID:3009023
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A,Map position: Xq27.1-Xq27.2
A,Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
                            R; Morita, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E. J. Biol. Chem. 260, 2583, 1985
A; Reference number. A37544
A; Reference number: A37544
A; Rontents: annotation; calcium binding, correction
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1018 TCTGAGAACATGCTGTGTGCGGGCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGCGAC 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               958 ITCATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTG 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 TyrLeuArgValProLeuValAspArgAlaThrCysLeuArgSerThrLysPheThrIle 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 ArgValPheHisLysGlyArgSer-----370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 GlyGluHisAsnIleGluGluThrGluHisThrGluGlnLysArgAsnValIleArglle 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 730 ITCGICCACCCCAACTACAGCAAGAGCACCACC----GACAAIGACAICGCACIGCIG 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 784 CACCIGGCCCAGCCCGCCACCTCICGCAGACCAIAGIGCCCAICTGCCTCCCGGACAGC 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 GluTyrThrAsnIlePheLeuLysPheGly-----SerGlyTyrValSerGlyTrpGly 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      904 -----TACCACAGCAGCCGAGAGGAGGACGCCAAGAAACCGCACCTTCGTCCTCAAC 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 PheAsnAspPheThrArgValValGlyGlyGluAspAlaLysProGlyGlnPheProTrp 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  550 CAGGIGGICCIGCIGGACICAAAGAAGAAGCIGGCCIGCGGGGCAGIGCICAICCACCCC 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 Glnvalval---LeuAsnGlyLysValAspAlaPheCysGlyGlySerIleValAsnGlu 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               610 ICCIGGGIGCIGACAGCGGCCCACIGCAIGGAIGAGICCAAGAAGCICCIIGICAGGCII 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ValSerValSerGlnThrSerLysLeuThrArgAlaGluAlaValPheProAspValAsp 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 TyrvalAsnSerThrGluAlaGluThrIleLeuAspAsnIleThrGlnSerThrGlnSer 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         549
                                              104 AsnGlyGlySerCySLySASpAspIleAsnSerTyrGluCysTrpCysProPheGlyPhe 123
                                                                                                         253 GAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTGGACAACGGCGGC 312
                                                                                                                                                             124 GluGIYLYSASnCYSGluLeuAspValThr-----CysAsnIleLysAsnGlyArg 140
                                                                                                                                                                                                                     313 TGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGG---CGCTGTAGCTGTGCGCCTGGC 369
                                                                                                                                                                                                                                                                             141 CysGluGInPheCysLysAsnSerAlaAspAsnLysValValCysSerCysThrGluGly 160
                                                                                                                                                                                                                                                                                                                                 370 TACAAGCTGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCTTGTGGGAGG 429
                                                                                                                                                                                                                                                                                                                                                                 844 GGCCTTGCAGAGCGCGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----CCGCGGCTCATTGATGGGAAGATGACCAGGCGGGGAGACAGCCCCTGG
193 GGGCACGCCACGTGCATCGACGCATCGGCAGCTTCAGCTGCGACTGCCGCAGCGGCTGG
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976 GICCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCTGAGAACATGCTGTGT 1035
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                                                                       370 TACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCTTGTGGGAGG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1096 GCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGGGGTGAGGCTGTGGG 1155
                                                                                                     169 AlaSerIleSerTyrSerSerLysLysIleThrArgAlaGluThrValPheSerAsnMet 188
                                                                                                                                                                                                                                       C.Species: Bos primigenius taurus (cattle)
C.Date: 30-Nov-1980 #sequence_revision 03-Aug-1984 #text_change 16-Jul-1999
                                                                                                                                                               --TGGAAGCGGATG 444
                                                                                                                                                                                                                                                                              189 AspTyrGluAsnSerThrGluAlaValPheIleGlnAspAspIleThrAspGlyAlaIle 208
                                                                                                                                                                                                                                                                                                                                                 580 CTGGCCTGCGGGCAGTGCTCATCCACCCCTCGTGGGTGCTGACAGCGGCCCACTGCATG 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 AlaPheCysGlyGlyAlaIleIleAsnGluLySTrpIleValThrAlaAlaHisCysLeu 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     640 GAIGAGICCAAGAAGCICCTIGICAGGCITGGAGAGIATGACCIGGGGCGCIGGGAGAAG 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 LysProGlyAspLysIleGluValValAlaGlyGluTyrAsnIleAspLysLysGluAsp 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  700 IGGGAGCIGGACCIGGACAICAAGGAGGICIICGICCACCCCAACIACAGCAAGAAGCACC 759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 ThrGluValGluGlyThrSerPheLeuThrGlyIleIleSerTrpGlyGluGluCysAla 434
                                                                                                                                                                                                                                                                                                                                                                                                     520 AAGATGACCAGGCGGGAGACAGCCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAG
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F;225-452/Domain: trypsin homology <TRY>
F;225-452/Domain: trypsin homology <TRY>
F;41.42,49,51,54,55,60,61,64,67,70,74/Modified site: gamma-carboxyglutamic acid (Glu) #s
F;52-57,85-96,90-105,107-116,122-133,129-143,145-158,166-333,250-266,380-394,405-433/Dis
F;265,313,409/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                              fac
                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Direct sequencing of the activation peptide and the catalytic domain of the A;Reference number: 146580; MUID:90152675; PMID:2303254
A;Accession: 149667
                                                                                                                  coagulation factor IXa (EC 3.4.21.22) precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Sate: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
C;Accession: JQ0419; 149667
R;Wu, S.M.; Stafford, D.W.; Ware, J.
Gene 86, 275-278, 1990
A;Title: Deduced amino acid sequence of mouse blood-coagulation factor IX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 GAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTCTGGTCCAAGCAC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 GGGCACGCCACGTGCATCGACGCCATCGGCAGCTTCAGCTGCGACTGCCGCAGCGGCTGG 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 GTCGACGGTGACCAGTGCTTTGGTCTTGGAGCACCCGTGCGCCAGCCTGTGCTGC 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 AsnGlyGlyIleCysLysAspAspIleSerSerTyrGluCysTrpCysGlnValGlyPhe 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 CTGGAGGAGCTCCGTCACAGCAGCCTGGAGCGGGAGTGCATAGAGGAGATCTGTGACTTC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 GluGluAlaArgGluValPheGluAsnThrGluLysThrThrGluPheTrpLysGlnTyr 79
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                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:M23109; NID:g193317; PIDN:AAA37629.1; PID:g387158
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Accession: JQ0419
Olecule type: mRNA
Residues: 1-459 <WUS>
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Mismatches:
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R; Sarkar, G.; Koeberl, D.D.; Sommer, S.S.
Genomics 6, 133-143, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-763-153-1 (1-1245) x JQ0419 (1-459)
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                                                                             RESULT 14
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A; Contents: annotation
A; Note: structure and location of a carbohydrate covalently bound to Ser
A; Note: structure and location of a carbohydrate covalently bound to Ser
C; Comment: Factor IX is activated by factor XIa, which excises the activation peptide py
C; Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strd
C; Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strd
C; Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strd
C; Function:
A; Description: catalyzes the proteolytic activation of coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C; Reywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F; 1-45, Domain: Gla domain homology (fragment) (GLA>
F; 1-45, Domain: EGF homology (Fragment) (GLA>
F; 182-146/Product: coagulation factor IXa heavy chain #status experimental (AHC>
F; 182-416/Product: coagulation factor IXa heavy chain #status experimental (Glu) #statis e. 409/Lomain: activation peptide #status experimental (AHC)
F; 181-181/20.21, 26, 27, 30, 33, 36, 40/Modified site: gamma-carboxyglutamic acid (Glu) #statis e. 556-71, 73-82, 88-99, 95-109, 111-124, 132-290, 207-223, 337-351, 362-390/Disulfide
F; 188-188, 168, 173, 261/Palnding site: carbohydrate (Asn) (covalent) #status experimental
F; 188, 168, 173, 261/Palnding site: carbohydrate (Asn) (covalent) #status experimental
F; 222, 270, 366/Active site: His, Asp, Ser #status predicted
C; Accession: A14757; B20274; I45891; A00923
R; Katayama, K.; Ericsson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Ti Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979
A; Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fa A; Reference number: A14757; MUD:80056619; PMID:291916
A; Recession: A14757
A; Molecule type: protein
A; Residues: 1-63, T', 65-416 < KAT>
B; McMullen, B.A.; Fulikawa, K.; Kisiel, W.
B; McGession: 192074
A; McGession: 1982
A; Title: Molecular cloning of the gene for human anti-haemophilic factor IX.
A; Reference number: 14589; MulD:82272386; PMID:6287289
A; Accession: 14589;
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A; Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coa. A; Reference number: A44556; WUID:89213999; PMID:3149637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 GICGACGGIGACCAGIGCTIGGICTIGCCCTIGGAGCACCCGIGCGCCAGCCIGIGCIGC 192
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Dlecule type: mRNA
Esidues: 52-139 <CHO>
Cross-references: GB:J00007; NID:g163053; PIDN:AAA30520.1; PID:g163054
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Indels:
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952 CTCAACTTCATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAAC 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 SerlleTyrSerHisMetPheCysAlaGlyTyrHisGluGlyGlyLysAspSerCysGln 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 AlaGlyGluHisAsnThrGluLysProGluProThrGluGlnLysArgAsnValIleArg 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   780
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                                                                                                                                                                                                                                                                313 TGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGG---CGCTGTAGCTGTGCGCCTGGC 369
                                                                                                                                                                                                                                                                                                                                                                                            370 TACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCTTGTGGGAGG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGAC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 AsnTyrGluAsnSerSerGluAlaGluIleIleTrpAspAsnValThrGlnSerAsnGln 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 SerPheAspGluPheSerArgValValGlyGlyGluAspAlaGluArgGlyGlnPhePro 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 GAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTGGACAACGGCGGC 312
                                                                                                                                                                                                                                                                                                                              95 CysLysGlnPheCysLysArgAspThrAspAsnLysValValCysSerCysThrAspGly 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 ValSerValSerHisIleSerLysLysLeuThrArgAlaGluThrIlePheSerAsnThr 154
193 GGGCACGGCACGTGCATCGACGCCATCGGCAGCTTCAGCTGCGACTGCCGCAGCGGCTGG 252
                                  58 AsnGlyGlyMetCysLysAspAspIleAsnSerTyrGluCysTrpCysGlnAlaGlyPhe 77
                                                                                                                                                                                          78 GluGlyThrAsnCysGluLeuAspAlaThr-----CysSerIleLysAsnGlyArg 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547 TGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGCTGGCCTGCGGGGCAGTGCTCATCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 TrpGln---ValLeuLeuHisGlyGluIleAlaAlaPheCysGlyGlySerIleValAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      667 CTTGGAGAGTATGACCTGCGGCGCTGGGAGAGTGGGAGCTGGACCTGGACATCAAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475 ACAGAAGACCAAGAAGACCAAGTAGAT------
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F;25-43/Domain: propeptide #status predicted <PRO>
F;28-87/Domain: Gla domain homology <GLA>
F;44-622/Product: prothrombin #status experimental <MAT>
F;44-327/Domain: activation peptide #status experimental <APT>
F;108-186/Domain: Aringle homology <FRI>
F;213-231/Domain: Aringle homology <FRI>
F;213-231/Domain: Aringle homology <FRI>
F;28-363/Product: thrombin light chain #status experimental <LCH>
F;38-463/Product: thrombin homology <FRI>
F;364-612/Product: thrombin homology <FRI>
F;364-612/Domain: trypsin homology <TRY>
F;364-613/Domain: trypsin homology <TRY>
F;49, 50, 57, 59, 62, 63, 68, 69, 72, 75/Modified site: gamma-carboxyglutamic acid (Glu) #statistion of the statistic statistic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F:391-407/Disulfide bonds: #status experimental
F:406.462/Active site: His, Asp #status predicted
F:416/Binding site: carbohydrate (Asn) (covalent) #status experimental
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29.09%
24.07%
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A; Residues: 1-622 <DEG>
A; Residues: 1-622 <DEG>
A; Residues: 1-622 <DEG>
A; Residues: 1-622 <DEG>
B; MA7262; GB:M33691; NID:g558069; PIDN:AAC63054.1; PID:g339641
B; Degen, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.
Biochemistry 22, 2087-2097, 1983
A; Title: Characterization of the complementary deoxyribonucleic acid and gene coding for A; Reference number: A00914; MUID:83231469; PMID:6305407
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A; Residues: 1-2, 'RI',5-100 <RES>
A; Cross-references: GB: M33011; NID:9190723; PIDN:AAA60220.1; PID:9190724
C; Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibri C; Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds ter 314-Arg, are released in natural blood clotting.
C; Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.
C; Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxyglutamyl residues bind calcium ions, result from the carboxyglutamyl charged phospholipid membrane surface.
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A; Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-
B; Rabiet, M.J.; Blashill, A.; Furie, B.C.
T.; Biol. Chem. 261, 13210-13215, 1986
Reference number: A37551; MUID: 87008532; PMID: 3759958
Contents: annotation; activation cleavages
Contents: annotation; activation cleavages
Ann. N. Y. Acad. Sci. 485, 73-9, 1986
A; Title: Recombinant genetic approaches to functional mapping of thrombin.
A; Reference number: 151952; MUID: 87182874; PMID: 3471151
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A'Residues: 44-118, N',120,'S',122-163,'I',165-175,'A',177-182,'T',184-193,'MV',196-308,
A'Residues: 44-118, N', Elion, J', Downing, M.R.; Mann, K.G.
J. Biol. Chem. 253, 4942-4957, 1977
A'Title: Primary structure of human prethrombin 2 and alpha-thrombin.
A'Reference number: A37550; MUID:77207112; PMID:873923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Map position: 11p11-11q12
A; Introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552
A; Introns: 27/1; 80/3; 89/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552
C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C; Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli
F;1-24/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Residues: 8-163,'N',165-622 <DE2>
A:Cross-references: GB:V00595; GB:J00307; NID:g37128; PIDN:CAA23842.1; PID:g1335344
                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Bate: 30-7800 #sequence_revision 22-Jul-1994 #text_change 08-Dec-2000
C;Accession: A29351; A00914; B00914; A37549; A37550; I51952
R;Degen, S.J.F; Davie, E.W.
Biochamitary 26, 6165-6177, 1987
Title: Nucleotide sequence of the gene for human prothrombin.
Reference number: A29351; MuID:88077877; PMID:2825773
Accession: A29351
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Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977
A;Reference number: A37549; MUID:77193964; PMID:266717
A;Accession: A37549
                                                                                                                                                                                                                                                                thrombin (EC 3.4.21.5) precursor [validated] - human
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                                                                                                                                                                                                                                                                                                                     N'Alternate names: coagulation factor II
N'Contains: prothrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: translated from GB/EMBL/DDBJ
1192 CGCTACCTCGACTGGATC 1209
                                                    404 ArgTyrValAsnTrpile 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 188-311 <DE3>
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61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 TrpAlaLysTyrThrAlaCysGluThrAlaArgThr---ProArgAspLysLeuAlaAla 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 AGCCIGIGCIGCGGCACGGCACGIGCAICGACGGCAICGGCAGC------ 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 ------CysLeuGluGlyAsnCysAlaGluGlyLeuGlyThrAsnTyrArgGlyHis 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 ValasnileThrargSerGlyIleGluCysGlnLeuTrpArgSerArgTyrProHisLys 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 ProGluIleAsnSerThrThrHisProGlyAlaAspLeuGlnGluAsnPhecysArgAsn 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACGAGCTGGAGCGGGAGTGCATAGAGGAG 60
                                                                                                                                                                                                                                                                                                                                      64 ThrCysSerTyrGluGluAlaPheGluAlaLeuGluSerSerThrAlaThrAspValPhe 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 ProAspSerSerThrThrGlyProTrpCysTyrThrThrAspProThrValArgArgGln 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 GluCysSerIleProValCysGlyGlnAspGlnValThrValAlaMetThrProArgSer 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 GAGGTGAGCTTCCTCAAT--------TGCTGCTGGACAACGGCGGC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 GlnTyrGlnGlyArgLeuAlaValThrThrHisGlyLeuProCysLeuAlaTrpAlaSer 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 AlaGlnAlaLysAlaLeuSerLysHisGlnAspPheAsnSerAlaValGlnLeuValGlu 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TACTGCCTA------GAGGAGGTGGGCTGCGGCGCGTGTAGCTGTGCG
                                                                                   622
169
62
161
189
24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 ---------TTCAGCTGCGAC-------
                                                                                                                                   Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------TGCACGCAT------
                                                                                                           Matches:
                                                                                                                                                                                   Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 -----AGCGGCTGGGAGGGCCGCTTCTGC----
F;568/Active site: Ser #status experimental
                                                                                                                                                                                                                                                      US-09-763-153-1 (1-1245) x TBHU (1-622)
                                                                             1.79e - 27
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613 Ile 613

οp	260	:::      AsnPheCysArgAsnProAspGlyAspGluGlyValTrpCysTyr 275	
οy	364	CCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTG 411	
qq	276	ValalaGlyLysProGlyAspPheGlyTyrCysAspLeuAsnTyrCysGluGluAlaVal 295	
οy	411	411	
qq	296	GluGluGluThrGlyAspGlyLeuAspGluAspSerAspArgAlaIleGluGlyArgThr 315	
δý	412	42	
qq	316		
οy	421	TGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGACACA 47	
qq	336		
à	478	GAAGACCAAGAAGACCAAGTAGATCGGGGCTCATTGATGGGAAGATGACCAGGCGGGGA 537 	
	538	GACAGCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGGAAGCTGGCCTGCGGGGCA 594	
οp	374	MetSerproTrpGlnValMetLeuPheArgLysSerProGlnGluLeuCysGlyAla 393	
Qy	595	GTGCTCATCCACCCCTCCTGGGTGCTGACAGCGGCCCACTGCATG639	
QQ	394	SerLeulleSerAspArgTrpValLeuThIAHIAHISCySLeuLeuTyrProProTrp 413	
Qy	640	GATGAGTCCAAGAAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGGGCGC 69	
οg	414		
م م	691	TGGGAGAAGTGGGAGCTGGACCTGGACATCAAGGAGGTCTTCGTCCACCCCAACTAC 747	
3 8	748	AGCAAGAGCACCACCGACAATGACATCGCACTGCTGCACCTGGCCCAGCCCGCCACC	
<sub>ි</sub> දු	454	ASDITPARGGIUASDLEUASPARGASPILEAIALEUMETLYSLEULYSLYSPROVALAIA 473	
ò	805		
. අ	474	:::	
Qy	865	AATCAGGCCGGCCAGGAGCCCTCGTGACGGGCTGGGGCTACCACAGCGAGAG 92	
qq	493		
à	922	AAGGAGGCCAAGAGAAACCGCACCTTCGTCAACTTCATCAAGATTCCCGTGGTCCCG 98	
	513	AlaAsnValGlyLysGlyGlnProSerValLeuGlnValValAsnLeuProIleValGlu 532	
ζ	982	CACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCTGAGAACATGCTGTGTGCGGGC 10	
qq	533	ArgProValCysLysAspSerThrArgIleArgIleThrAspAsnMetPheCysAlaG1Y 332	
Qy	1042	ATCCTCGGGGACCGCAGGATGCCTGCGAGGGGGGGACAGTGGGGGGCCCATG 10	
Ср	553	TyrLysProAspGluGlyLysArgGlyAspAlaCysGluGlyAspSerGlyG1yFroPhe >/2	
δy	1093	GTCGCCTCCTTCCACGCCACCTGGTTCCTGGTGGGCCTGGTGAGCTGGGGTGAG	
g	573	29.0	
δ. Q.	1147	7 GGCTGTGGGCTCCTTCACAACTACGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGG 1206 	
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F;44-199/Domain: activation peptide 1 #status experimental <FR1>
F:109-187/Domain: kringle homology <KR1>
F:200-317/Domain: activation peptide 2 #status experimental <FR2>
F:200-317/Domain: activation peptide 2 #status experimental <FR2>
F:214-292/Domain: kringle homology <KR2>
F:318-366/Product: thrombin light chain #status experimental <LCH>
F:367-625/Product: thrombin heavy chain #status experimental <HCH>
F:367-616/Domain: trypsin homology <FR2>
F:367-616/Domain: trypsin homology <FR2>
F:367-616/S1.58.60, 63.64, 69.70, 73.76/Modified site: gamm-carboxyglutamic acid (Glu) #status
F:60.51.58.60, 63.64, 69.70, 73.76/Modified site: gamm-carboxyglutamic acid (Glu) #status
F:10.144,419/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:409,465,571/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 TTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACTGGCCTTCTGGTCCAAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 CACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCCAGCCTGTGC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 TyrThrAlaCysGluSerAla------ArgAsnProArgGluLysLeuAsn 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 ---TGCGGGCACGGCACGTGCATCGACGCCATC-------GGCAGCTTCAGC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 TGCGACTGCCGCAGCGGC------260GAGGGCCGC-----261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 Val---ThrargSerGlyIleGluCysGlnLeuTrpArgSerArgTyrProHisLysPro 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 GlulleAsnSerThrThrHisProGlyAlaAspLeuArgGluAsnPheCysArgAsnPro 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----- 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 AspGlySerIleThrGlyProTrpCysTyrThrThrSerProThrLeuArgArgGluGlu 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AACGGC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 CysSerValProValCysGlyGlnAspArgValThrValGluValIleProArgSerGly 201
                                                                                                                                                                                                                                                                                                                                                                                                                68 ArgGluGluAlaPheGluAlaLeuGluSerLeuSerAlaThrAspAlaPheTrpAlaLys 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 GlyserThrThrSerGlnSerProLeuLeuGluThrCysValProAspArgGlyArgGlu 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 TyrargGlyArgLeuAlaValThrThrSerGlySerArgCysLeuAlaTrpSerSerGlu 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 GlnAlaLysAlaLeuSerLysAspGlnAspPheAsnProAlaValProLeuAlaGluAsn 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 TACTGCCTA------GAGGAGGTGGGCTGGCGGCGCTGTAGCTGTGCGCCT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CAT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 PheCysArgAsnProAspGlyAspGluGluGlyAlaTrpCysTyrValAlaAspGlnPro 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 GlyAspPheGluTyrCysAspLeuAsnTyrCysGluGluProValAspGlyAspLeuGly 301
                                                                                                                                                                                                                                                                                                                                                                                        10 TICCIGGAGGAGCICCGICACAGCAGCCIGGAGCGGGAGIGCAIAGAGGAGAICIGIGAC
                                                                                                                                                                                                                                           625
168
62
152
205
23
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                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                            Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 GTGAGCTTCCTCAATTGCTCGCTGGAC-------
                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                   US-09-763-153-1 (1-1245) x TBBO (1-625)
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412 ------AAGTTCCCTTGTGGG--- 426
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                                                   302 AspArgLeuGlyGluAspProAspProAspAlaAlaIleGluGlyArgThrSerGluAsp 321
                                                                                                                                                                 322 HisPheGlnProPhePheAsnGluLysThrPheGlyAlaGlyGluAlaAspCysGlyLeu 341
                                                                                                                                                                                                                           427 AGGCCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGACACAGAAGACCAA 486
                                                                                                                                                                                                                                                                                  342 ArgPro-----LeuPheGluLysLysGlnValGlnAspGlnThrGluLysGluLeuPhe 359
                                                                                                                                                                                                                                                                                                                                                                                         360 GluSerTyrIleGluGlyArgIleValGluGlyGlnAspAlaGluValGlyLeuSerPro 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                         547 IGGCAGGIGGICCTGCIG---GACICAAAGAAGAAGCIGGCCTGCGGGGCCAGTGCICAIC 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 SerAspArgTrpValLeuThrAlaAlaHisCysLeuLeuTyrProProTrpAspLysAsn 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1075 GACAGIGGGGGCCCAIGGIC-----GCCICCIICCACGGCACCIGGIICCIGGIGGGC 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1129 CTGGTGAGCTGGGGTGAGGCTGTGGGCTTCACAACTACGGCGTTTACACCAAAGTC 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          649 ----AAGAAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGGCGCTGGGAG--- 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420 PheThrValAspAspLeuLeuValArgIleGlyLysHisSerArgThrArgTyrGluArg 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              697 AAGTGGGAGCTGGACCTGGACATCAAGGAGGTCTTCGTCCACCCCCAACTACAGC---AAG 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                754 AGCACCACGACAATGACATCGCACTGCTGCACCTGGCCCAGCCGGCACCTCTCGCAG 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 GluasnLeuAspArgAspIleAlaLeuLeuLysLeuLysArgProIleGluLeuSerAsp 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             814 ACCATAGTGCCCATCTGCCTCCCGGACAGCGGCCTTGCAGAGCGCGAGCTCAATCAGGCC 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          874 GGCCAGGAGACCCTCGTGACGGGCTGGGGCTACCACAGCAGCCGAGAAGGAGGAGCCAAG 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               510 ArgArgGluThrTrpThrThrSerValAlaGluValGlnProSerValLeuGlnValVal 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            530 AsnLeuProLeuValGluArgProValCysLysAlaSerThrArglleArglleThrAsp 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -------9TCCTCAACTTCATC 963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GATGAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         604 CACCCTCCTGGGTGCTGACAGCGGCCCACTGCATG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombin (EC 3.4.21.5) precursor - mouse C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              934 AGAAACCGCACCTTC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1189 AGCCGCTACCTCGACTGGATC 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610 PheArgLeuLysLysTrplle 616
411
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967 ATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCTGAGAAC 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 916 CGAGAG-----AAGGAGGCCAAGAGAAACCGCACCTTCGTCCTCAACTTCATCAAG 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    796 CCCGCCACCCTCTCGCAGACCATAGTGCCCATCTGCCTCCCGGACAGGGGCCTTGCAGAG 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468 ProValProPheSerAspTyrIleHisProValCysLeuProAspLysGlnThrVal--- 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              487 ThrSerLeuLeuArgAlaGlyTyrLysGlyArgValThrGlyTrpGly-----AsnLeu 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   428 ArgThrArgTyrGluArgAsnValGluLysIleSerMetLeuGluLysIleTyrValHis 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           739 CCCAACTACAGC---AAGAGCACCACCGACAATGACATCGCACTGCTGCTGCACCTGGCCCAG 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         586 recegegeagrecrearceaccecreegrecreacagegeccacrecarg---- 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 -----GATGAGICC-----AAGAAGCICCTIGICAGGCTIGGAGAGTATGAC 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 682 CIGCGGCGCIGGGAGAAG---TGGGAGCIGGACCIGGACAICAAGGAGGICTICGICCAC 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 ThrThrAspAlaGluPheHisThrPhePheAsnGluLysThrPheGlyLeuGlyGluAla 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTTGTGGG---AGGCCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGAC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           475 ACAGAAGACCAA-----GAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACC 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 ThrGluLysGluLeuLeuAspSerTyrIleAspGlyArgIleValGluGlyTrpAspAla 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 AGCTICCICAATIGCICGCIGGACAACGGCGGCIGCACGCATIACIGCCIAGAGGAGGIG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340 GGCTGGCGGCGCTGTAGCTGTGCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGT 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 Gly-------GluGluAsnTyrAspValAspGluSerIleAlaGlyArg 311
                                                                                                                                                                                                                                          224 GlnGlyAsnLeuAlaValThrThrLeuGlySerProCysLeuProTrpAsnSerLeuPro 243
                                                                                                                                                                                                                                                                                                                                             244 AlaLysThrLeuSerLysTyrGlnAspPheAspProGluValLysLeuValGluAsnPhe 263
                                                                                                                                                                                                                                                                                                                                                                                             238 TGCCGCAGC---GGCTGG-----GAGGGCCGCTTCTGCCAG------CGCGAGGTG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                284 AspPheGluTyrCysAsnLeu--------AsnTyrCysGluGluAlaVal 297
                                     184 ValProValCysGlyGlnGluGlyArgThrThrValValWatThrProArgSerGlyGly 203
                                                                                        ------ GGCACGTGCATCGACGCCATCGCC----- 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 AspCysGlyLeuArgPro----LeuPheGluLysLys-----SerLeuLysAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              529 AGGCGGGGAGACAGCCCCTGGCAGGTGGTCCTGCTG---GACTCAAAGAAGAAGCTGGCC
                                                                                                                                        204 SerLysAspAsnLeuSerProProLeuGlyGlnCysLeuThrGluArgGlyArgLeuTyr
                                                                                                                                                                                                                                                                                                     400 CACCCCCCAGTGAAGTTC--------
  181 AGCCTGTGCTGCGGGCAC--
                                                                                                        199 -----
                                                                                                                                                                                                        222 -----
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F;50,51,58,60,63,64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F;61-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-547,5
F;403,459,565/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                A; Molecule Lype: mRNA
A; Molecule Lype: mRNA
A; Residues: 1-618 ocnos:
A; Residues: 1-618 ocnos: Strain C57BL/6
A; Experimental source: strain C57BL/6
A; Note: the data were obtained from females resulting from the cross of M. domesticus an
B; Banfield, D.K.; MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A; Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A; Reference number: A42696; MUID:92212913; PMID:1557383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Residues: 384-618, E' CBAN>
ross-references: GBNB1394
uperfamily: thrombin; GB domain homology; kringle homology; trypsin homology
uperfamily: thrombin; calcium binding; carboxyglutamic acid; glycoprotein; hydr
Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr
F: 1-24/Domain: slgnal sequence #status predicted <SIG>
F: 25-43/Domain: propeptide #status predicted <PRO>
F: 28-88/Domain: Gla domain homology <GLA>
C; Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 03-May-2002 C; Accession: A35827; A42696; S12081 R; Degen, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pai, J.A. DNA Cell Biol. 9, 487-498, 1990 A; Title: Characterization of the CDNA coding for mouse prothrombin and localization of the A; Reference number: A35827; MUID: 9102551; PMID: 2222810 A; A35827 A; MUID: 9102551; PMID: 2222810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 SerThrThrGlyProTrpCysTyrThrThrAspProThrValArgArgGluGluCysSer 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 ThrHisThrGlyIleGlnCysGlnLeuTrpArgSerArgTyrProHisLysProGluIle 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----1GCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheTrpAlaLysTyrThrValCysAspSerValArgLysProArgGluThrPheMetAsp 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 CysLeuGluGlyArgCysAlaMetAspLeuGlyValAsnTyrLeuGlyThrValAsnVal 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 -----GACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCG------- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCAACTCC---TTCCTGGAGGAGCTCCGTCACAGCAGCCTGGAGCGGGAGTGCATAGAG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluGlnCysSerTyrGluGluAlaPheGluAlaLeuGluSerProGlnAspThrAspVal
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1167
65
1152
202
27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F:14-618/Product: prothrombin B #status predicted <WAT>F:109-187/Domain: kringle homology <KR1>F:215-293/Domain: kringle homology <KR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 TTCTGGTCCAAGCACGTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        533.00
39.59%
28.50%
22.81%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary A; Molecule type: mRNA
                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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GAGATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCC 117
                                                                                                                                                                                                                   84 PheTrpAlaLysTyrThrValCysAspSerValArgLysProArgGluThrPheMetAsp 103
                                                                                                                                                                                                                                                                                                                                                         104 CysieuGluGlyArgCysAlaMetAspLeuGlyLeuAsnTyrHisGlyAsnValSerVal 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 ThrHisThrGlyIleGluCysGlnLeuTrpArgSerArgTyrProHisArgProAspIle 143
                                                         44 AlaAsnSerGlyPheLeuGluGluLeuArgLysGlyAsnLeuGluArgGluCysValGlu 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCCAACTCC---TTCCTGGAGGAGCTCCGTCACAGCAGCCTGGAGCGGGAGTGCATAGAG 57
                                                                                                                                                       157 TTGCCCTTGGAGCACCCGTGCGCCAGCCTG-----TGCTGCGGGCAGGCACG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 SerThrSerGlyProTrpCysTyrThrThrAspProThrValArgArgGluGluCysSer 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 -----AGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 SerLysGluAsnLeuSerProProLeuGlyGluCysLeuLeuGluArgGlyArgLeuTyr 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 GlnGlyAsnLeuAlaValThrThrLeuGlySerProCysLeuAlaTrpAspSerLeuPro 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 ThrLysThrLeuSerLysTyrGlnAsnPheAspProGluValLysLeuValGlnAsnPhe 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 TGCCTA------GAGGAGGTGGGCTGGCGGCGCTGTAGCTGTGCGCCTGGC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||
| 264 CysargasnProaspargaspdluGluGlyAlaTrpCysPheValalaGlnGlnProGly 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ACGCATTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 PheGluTyr---CysSerLeuAsnTyrCysAspGluAlaVaiGlyGluGluAsnH1sAsp 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 GlyAspGluSerIleAlaGlyArgThrThrAspAlaGluPheHisThrPhePheAspGlu 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         412 ------AAGTTCCCTTGTGGG---AGGCCCTGGAAGCGGATGGAGAG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 ArgThrPheGlyLeuGlyGluAlaAspCysGlyLeuArgPro----LeuPheGluLys 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 AAGCGCAGTCACCTGAAACGAGACACAGAAGACCAAGAAGACCAAGTAGATCCGCGGCTC 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 LysSerLeuThrAspLysThrGluLysGluLeuLeuAspSerTyrIleAspGlyArglle 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               511 ATTGATGGGAAGATGACCAGGGGGGGAGACAGCCCTTGGCAGGTGGTCCTGCTG---GAC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 ValGluGlyTrpAspAlaGluLysGlylleAlaProTrpGlnValMetLeuPheArgLys 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           568 TCAAAGAAGAAGCTGGCGTGCGGGGCAGTGCTCATCCACCCCTCGTGGGTGCTGACAGCG 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 TACAAGCTGGGGACGACCTCCTGCAGTGTCACCCCGCAGTG-----
                                                                                                                                                                                                                                                                                                               148 TGCTTG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombin (EC 3.4.21.5) precursor - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 07-Way-1993 #text_change 03-May-2002
C; Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 03-May-2002
C; Date: 07-Way-1993 #sequence_revision 07-May-1993 #text_change 03-May-2002
C; Date: 08-Way-1993 #sequence_revision 07-May-1993 #text_change 03-May-2002
C; Date: 08-Way-1993 #sequence 08-Way-1993 #text_change 03-May-2002
C; Date: 08-Way-1993 #sequence 08-Way-1993
C; Date: 08-Way-1993 #sequence 08-Way-1993
A; Title: CDNA sequence 0 frat prothrombin
A; Recession: S10511; MUD: 90332426; PMID: 2377469
A; Molecule type: MRNA
A; Residues: 1-617 < CHB-
A; Cross-references: EMBL: X52835; NID: 956969; PIDN: CAA37017.1; PID: 956970
Badocarinology 126, 167-175, 1990
A; Reference number: A60576; MUD: 90091942; PMID: 2293980
A; Reference number: A60576; MUD: 90091942; PMID: 2293980
A; Molecule type: Protein
A; Residues: 44-58 CHENA
A; Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute
B; Ranifield, D.K.; MadGilliyray, R.T.A.
A; Title: Partial characterization of verrebrate prothrombin cDNAs: amplification and sequence number: A42696; MUD: 92212913; PMID: 1557383
A; Reference number: A42696; MUD: 92212913; PMID: 1557383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C; Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr
F;1-24/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;25-43/Domain: propeptide #status predicted <PRO>F;28-88/Domain: propeptide #status predicted <PRO>F;28-88/Domain: Gla domain homology <GLA>F;28-88/Domain: Gla domain homology <GLA>F;28-88/Domain: kringle homology <RR1>F;215-292/Domain: kringle homology <RR2>F;305-609/Domain: trypsin homology <RR2>F;306-609/Domain: trypsin homology <RR2>F;50.51.58,60,63.64,69,70,73,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F;61-66,91-104,109-187,130-170,158-182,236-276,264-287,332-478,387-403,532-546,97402,458,564/Active site: His, Asp, Ser #status predicted
                                                                   1027 ATGCTGTGTGCGGGATC---CTCGGGGAC-----CGGCAGGATGCCTGCGAGGGGGAC 1077
                                                                                                                                                          1078 AGIGGGGGCCCAIGGIC----GCCICCIICCACGGCACCIGGIICCIGGIGGGCCIG 1131
                                                                                                                                                                                                                                                      1132 GIGAGCIGGGGIGAGGGCIGIGGGCICCTICACAACIACGGCGIITACACCAAAGICAGC 1191
:::|||:::||||
525 LeuProlleValGluArgProValCysLysAlaSerThrArgIleArgIleThrAspAsn 544
                                                                                                565 SerdlyGlyProPheValMetLysSerProPheAsnAsnArgTrpTyrGlnMetGlyIIe 584
                                                                                                                                                                                                                                                                                 Conservative:
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Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                             1192 CGCTACCTCGACTGGATC 1209
                                                                                                                                                                                                                                                                                                                                                                                              605 ArgLeuLysArgTrp1le 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.57e-25
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40.21%
28.85%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: mRNA
Residues: 383-617,'E' <BAN>
(Cross-references: GB:M81397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.49%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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628 GCCCACTGCATG------GATGAGTCC-----AAGAAGCTCCTTGTC 663

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F;202-237/Domain: fibronectin type I repeat homology <1Fl>
F;245-278/Domain: EGF homology <EG2>
F;245-278/Domain: Kringle homology <KRG>
F;356-367/Domain: kringle homology <KRG>
F;373-407/Product: hepatocyte growth factor activator light chain #status experimenta F;408-655/Product: hepatocyte growth factor activator heavy chain #status experimenta
                                                                                                                                      F;468-641/Domain: trypsin homology <TRY>
F;40.48,290,468,492,546/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;40,48,290,468,402,546/Binding site: carbohydrate (Asn) (269-278,286-367,307-349,338
F;164-175,169-186,188-197,202-230,228-237,245-256,250-267,269-278,286-367,307-349,338
F;447,497,598/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 GACCAAGAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGGGGAGAC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 AGCCCCIGG-----CAGGIGGICCTGCIGGACTCAAAGAAGAAGTGGCCIGCGGGGCA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 HisprotrpLeuAlaAlaIleTyrIleGlyAspSer------pheCysAlaGly 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTACCCCGCAGTGAAGTTCCCT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 TGTGGGAGGCCCTGGAAGCGGATGGAGAAGCGCAGTCACCTGAAACGAGACACAGAA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 LeuGlyLeuGlyProHisAlaTyrCysArgAsnProAspAsnAspGluArgProTrpCys 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 TyrvalvallysAspSerAlaLeuSerTrpGluTyrCysArgLeuGluAlaCysGluSer 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 AGCGGCTGGGAGGCCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTGGAC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 ProGlyPheAladlyArgLeuCysAsnIleGluProAsp---GluArgCysPheLeuGly 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 -----GlyGlyThrCySHisLeuileValAlaThrGlyThrThrValCySAlaCySPro 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 AspargIrpAlaArgValArgGlnGlyHisValGluGlnCysGluCysPheGlyGlyArg 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 ThrTrpCysGluGlyThrArgHisThrAlaCysLeuSerSerProCysLeuAsn---- 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 CGGGAGIGCATAGAGGAGATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 LysaspCysGlyThrGluLysCysPheaspGluThrargTyrGluTyrLeuGluGlyGly 214
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A;Description: activates hepatocyte growth factor by specific proteolytic cleavage
A;Description: activates negeneration
C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C;Keywords: glycoprotein; hydrolase; Kringle; liver; plasma; serine proteinase
C;Keywords: glycoprotein; hydrolase; kringle; liver; plasma; serine proteinase
F;134,Pomain: signal sequence #status predicted <SIG>
F;108-148/Domain: fibronectin type II repeat homology <1F2>
F;164-197/Domain: EGF homology <EG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;MIyazawa, K.; Shimomura, T.; Kitamura, A.; Kondo, J.; Morimoto, Y.; Kitamura, N. J. Biol. Chem. 268, 10024-10028, 1993
Title: Molecular cloning and sequence analysis of the cDNA for a human serine protease oggulation factor XII.
Ference number: A46688; MUID:93252878; PMID:7683665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: DDBJ:D14012; NID:g219680; PIDN:BAA03113.1; PID:g219681
A; Experimental source: liver (mRNA); serum (protein)
A; Note: sequence extracted from NCBI backbone (NCBIN:131227, NCBIP:131228)
A; Note: parts of the sequence, including the amino ends of the heavy and light chains, C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hepatocyte growth factor activator (EC 3.4.21.-) precursor [validated] - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 25-Aug-1995 #text_change 08-Dec-2000
C;Accession: A46688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1114 TGGIICCIGGIGGGCCIGGIGAGCIGGGGIGAGGCIGIGGGCTCTICACAACIACGGC 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1009 AACAIGGIGICIGAGAACAIGCIGIGIGGGGCAIC---CICGGGGAC-----CGGCAG 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1060 GATGCCTGCGAGGGGGACAGTGGGGGGCCCATGGTC-----GCCTCCTTCCACGGCACC 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     949 GTCCTCAACTTCATCAAGAITCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGC 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              538 IleArg1leThrAspAsnMetPheCysAlaGlyPheLysValAsnAspThrLysArgGly 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 AspLysGlnThrVal---ThrSerLeuLeuGlnAlaGlyTyrLysGlyArgValThrGly 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 898 IGGGGCTACCACAGCAGCCGAGAG-----AAGGAGGCCAAGAGAAACCGCACCTTC 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  500 TrpGly-----AsnLeuArgGluThrTrpThrThrAsnIleAsnGluIleGlnProSer 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 valleuGlnValValAsnLeuProIleValGluArgProValCysLysAlaSerThrArg 537
                                                                                                                                                                                                                                                                                                                                                                         461 LeuLeuLysLeuLysLysProValProPheSerAspTyrIleHisProValCysLeuPro 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 GluLysileTyrileHisProArgTyrAsnTrpArgGluAsnLeuAspArgAspIleAla 460
                                                                                                                                                                                                                                                                                                                                            778 CTGCTGCACCTGGCCCAGCCCGCCTCTCGCAGACCATAGTGCCCCATCTGCCTCCCG 837
                                                                                                                                                                            421 ArgilediyLysHisSerArgThrArgTyrGluArgAsnValGluLysIleSerMetLeu 440
                                                                                                                                                                                                                                  721 AAGGAGGTCTTCGTCCACCCCAACTACAGC---AAGAGCACCACCGACAATGACATCGCA 777
                                                               |||||||||||::
401 AlaHisCysIleLeuTyrProProTrpAspLysAsnPheThrGluAsnAspLeuLeuVal 420
                                                                                                                        664 AGGCITGGAGAGIATGACCTGCGGCGCTGGGAGAAG---TGGGAGCTGGACCTGGACATC 720
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                                                         A)Gene: GDB:HGFAC; HGFA; HGFAP
A)Cross-references: GDB:9954514
A)Map position: 4P16-4P16
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A; Residues: 1-655 <MIY>
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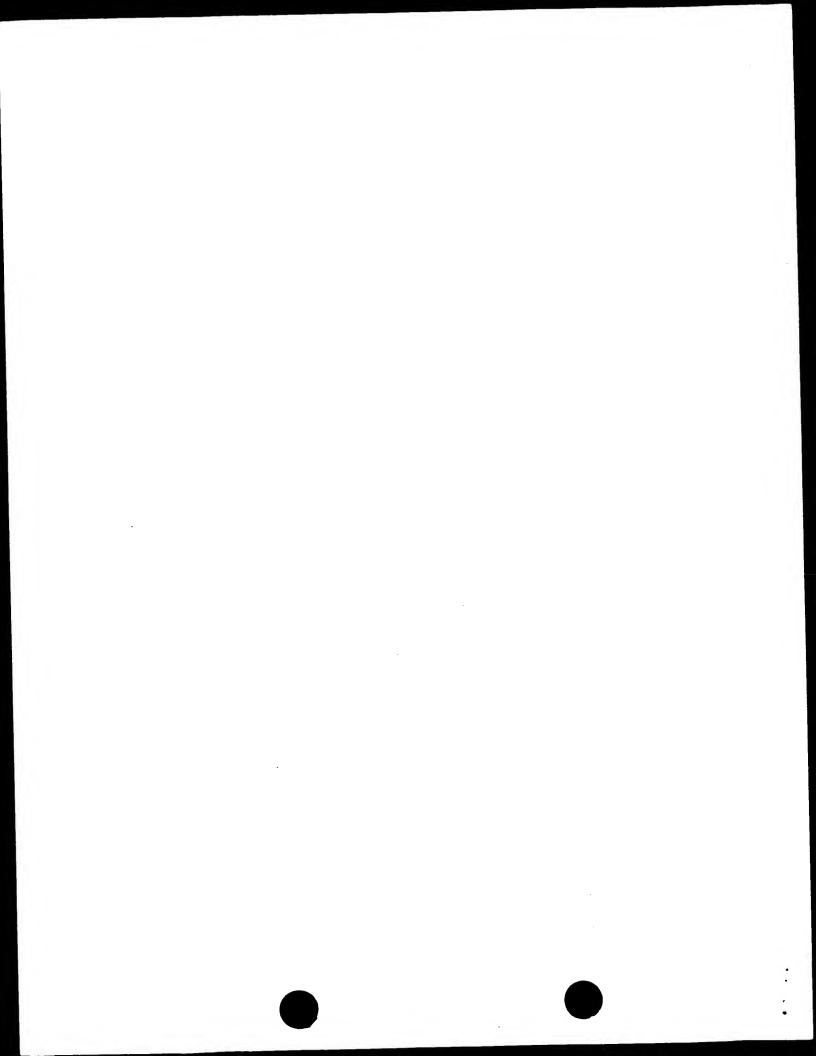
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| 435 SerLeuValHisThrCysTrpValValSerAlaAlaHisCysPheSerHisSerProPro 454
                                      649 ---AAGAAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGGCGCTGGGAGAAGTGGGAG 705
                                                                                                                                                                                                                                                                                                                                                               970 CCCGTGGTCCCGCACAATGAGTGCAGC-----GAGGTCATGAGCAACATGGTGTCTGAG 1023
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                                                       455 ArgAspSerValSerValValLeuGlyGlnHisPhePheAsnArgThrThrAspValThr 474
                                                                                         706 CTGGACCTGGACATCAAGGAGGTCTTCGTCCACCCCAACTACAGCAAG---AGCACCACC 762
                                                                                                                                              763 GACAATGACATGGCACTGCACCTGGCCCAGCCC------GCCACCCTCTCG 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1084 GGGCCCATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGGGGT 1143
                                                                                                             475 GlnThrPheGlylleGluLysTyrIleProTyrThrLeufyrSerValPheAsnProSer 494
                                                                                                                                                               811 CAGACCATAGIGCCCATCIGCCICCGGACAGGGGCCTIGCAGAGGGGGGGGGTCAATCAG 870
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| 560 ProLeuValAlaAspHisLysCysSerSerProGluValTyrGlyAlaAspIleSerPro 579
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atabase : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	PRIC HIMAN	F0#0/0	178861 000	PRTC BOVIN	F00/43	F31594		22820	019045		P98139		FAIU_HUMAN P00742 homo sapien	HUMAN P08709 homo sapien	BOVIN P22457 hos taning		0,000	P19340	POU/40 nomo sapien	A MOTISE
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 60 summaries

Command line parameters:

## ALIGNMENTS

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"Protein C deficiency: a database of mutations. For the Protein C & Subcommittee of the Scientific and Standardization Committee of the International Society on Thrombosis and Haemostasis.";
Thromb. Haemost. 69:77-84(1993).
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MEDLINE~90293094; PubMed=1694179;
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MEDLINE=93190290; PubMed=8446940;
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MEDLINE-92276939; PubMed=1593215;
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TSAY W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C., Koerper M.A., Coughlin J., Griffin J.H., "Genetic mutations in ten unrelated American patients with
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Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
"Symptomatic type II protein C deficiency caused by a missense
mutation (Gly 381-->Ser) in the substrate-binding pocket.";
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MEDLINE-94122329; Pubmed-8292730;
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Mismatches:
with hereditary protein C deficiency.";
Blood Coagul. Fibrinolysis 4:273-280(1993).
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Blood Coagul. Fibrinolysis 4:791-796(1993).
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Shen L., He X., Dahlback B.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VILIA
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15-DEC-1998 (Rel. 37, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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SO SELLE BELLE BEL
                                                                                       C. -- SUBDNITE: SYTTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE BUXBARE IS THEN ACTIVATED BY THROMEN, WHICH CLEAVES A TETRADECAPEPETIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLEY PROMOTED BY THROMEOMODILIN.

C. --- PTH. THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROPERTY TO BIND CALLOTOM.

ANOTHER SITE, BEYOND THE GLO DOMAIN. THIS GLA-INDEPENDENT BINDING STITE IS NECESSARY FOR THE RECOGNITION OF THE THROMEOMODILIN COMPLEX.

THROMENOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING STITE IS NECESSARY FOR THE RECOGNITION OF THE THROMEOMODILIN COMPLEX.

THROMEN THROMEOMODILIN COMPLEX.

THROMEN THROMEOMODILIN COMPLEX.

SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMEOMODILIN COMPLEX.

THROMEN THROMEOMODILIN COMPLEX.

--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROTEIN C LIGHT CHAIN (BY SIMILARITY).
PROTEIN C HEAVY CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
                                -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAMMA-CARBOXYGLUTAMIC ACID
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   IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
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PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS010021; EGE_1; 1.
PROSITE; PS01186; EGE_2; 2.
PROSITE; PS01187; EGE_CA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS000134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001881; EGF_Ca.
InterPro; IPR001254; Ser_Drotease_Try.
InterPro; IPR001254; Ser_Drotease_Try.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF00594; glas; 1.
SMART; SM00181; EGF; 2.
SWART; SM00069; GLA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF-LIKE 1.
EGF-LIKE 2.
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InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U49933; AAA92956.1; -. HSSP; P04070; 1PCU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 HisGlyGlyTrpGluGlySerPheCysGlnTyrGluValArgPheSerAsnCysSerVal 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
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                                                                                                                                                                                                                                                                             DY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLÜNAC. . .) (POTENTIAL).

N-LINKED (GLÜNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. .) (POTENTIAL)
D75A5F990C8F29D7 CRC64;
                                                                                                         HYDROXYLATION (BY SIMILARITY).
CHARGE RELAY SYSTEM.
CHARGE RELAX SYSTEM.
CHARGE RELAX SYSTEM.
                                                                    (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
                          GAMMA-CARBOXYGLUTAMIC ACID
                                                GAMMA-CARBOXYGLUTAMIC ACID
GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
                                                                                             (BY SIMILARITY).
                                                                                                                                                                 BY SIMILARITY.
                                         (BY SIMILARITY)
              (BY SIMILARITY)
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Best Local Similarity:
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952 CTCAACTTCATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAAC 1011
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197 GluGlnValAspGluMetAspGluValAspProArgLeuIleAspGlyLySLeuThrArg 216
                                                                                                 1132 GTGAGCTGGGGTGAGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGC 1191
                                                                                                                                                                                                       CIGGACATCAAGGAGGTCTTCGTCCACCCCAACTACAGCAGCAGCACCACCGACAATGAC 771
                                                                                                                                                                                                                                                                                                                                                           ACGGGCTGGGGCTACCACAGCAGCCGAGAGAAGGAGGCCAAGAGAAACCGCACCTTCGTC 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Porcine factor V: cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anatomy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
Kim H.K.W.;
                          532 CGGGGAGACAGCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGTGGCCTGCGGG
                                        GCAGTGCTCATCCACCCCTCCTGGGTGCTGACAGCGGCCCACTGCATGATGAGTCCAAG
                                                                                                                                       AAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGGCGCTGGGAGAAGTGGGAGCTGGAC
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15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
                                                                                                                                                                                                                                                772 ATCGCACTGCTGCACCTGGCCCAGCCCGCCACCTCTCGCAGACCATAGTGCCCATCTGC
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                               "SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.

-I ISSUE SPECIFICITY: Plasma; synthesized in the liver.
-I FTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
-I MISCELLANGOUS: carcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the trombin-thrombomodulin complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blood coagulation; Glycoprotein; Serine protease;
Gamma-carboxygultanic acid; Calcium-blinding; Vitamin K; Hydroxylation;
BGF-like domain; Repeat; Endothelial cell: Hydrolase; Sinnal
             Cell. Mol. Life Sci. 58:148-159(2001).
-!-FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of Calcium ions and phospholipids.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
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19 41 BY SIMILARITY.
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PRIMIS; PRO0722; CHYMOTRYPSIN.
PRIMIS; PRO0722; CHYMOTRYPSIN.
PRIMIS; PRO0722; CHYMOTRYPSIN.
SMART; SMO0181; EGF; 2.
SMART; SMO0019; EGF; 1.
PROSTIE; PS00020; TryP_SPC; 1.
PROSTIE; PS00020; EGF_1; 1.
PROSTIE; PS01180; EGF_2; 2.
PROSTIE; PS01187; EGF_2; 2.
PROSTIE; PS01187; EGF_CA; 1.
PROSTIE; PS001137; TRYPSIN_IDM; 1.
PROSTIE; PS001134; TRYPSIN_IDM; 1.
PROSTIE; PS00134; TRYPSIN_IDM; 1.
PROSTIE; PS00134; TRYPSIN_IDM; 1.
PROSTIE; PS00134; TRYPSIN_IDM; 1.
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InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001814; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR002383; GIA_blood.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001294; VitK_dep_GIA.
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EGF-LIKE 2.
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Pfam; PF00089; trypsin; 1.
Pfam; PF00594; gla; 1.
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INTERCHAIN (BY SIMILARITY).
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Bos taurus (Bovine)

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13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 04), Last ennotation update)
Vitamin-K dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
                                                   202 GlnValaspLysLysGluAspGlnIleAspProArgLeuValAsnGlyLysGlnSerPro
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SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE BUXZME IS THEN ACTIVATED BY THROWENIN, WHICH CLEAVES A FERRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS STRONGLY PROMOTED BY THROMBONDOULIN.

TISSUE SPECIFICITY: PLASMA, SYNTHESIZED IN THE LIVER.

FTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME MISCELLANEOUS: CALCIUM.

MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLAD DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE READ DOMAIN. THIS GLA-INDEPENDENT BINDING SITE.
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MEDLINE-83213513; PubMed-6304092;
Esmon N.L., Debault L.E., Esmon C.T.;
"Proteolytic formation and properties of gamma-carboxyglutamic acid-
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                          MEDLINE-85014826; PubMed-6091100;
Long G.L., Baldagale R.M., McGillivray R.T.A.;
"Cloning and sequencing of liver cDNA coding for bovine protein C.
Proc. Natl. Acad. Sci. 0.5.A. 81:5653-5656(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drakenberg T., Fernlund P., Roepstorff P., Stenflo J., "Beta-hydroxyaspartic acid in vitamin K-dependent protein C.", Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-83007326; PubMed-6896877; Stenflo J., Fernlund P.; "Amino acid sequence of the heavy chain of bovine protein C."; J. Biol. Chem. 257:12180-12190(1982).
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-83007325; Pubmed-6896876; Ferning P. Stenfio J.; Annino acid sequence of the light chain of bovine protein C."; J. Biol. Chem. 257:12170-12179(1982).
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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MEDLINE-83213514; PubMed-6406503;
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J. Biol. Chem. 258:5548-5553(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-83169769; PubMed-6572939;
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 40-194.
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISION TO 110.
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EMBL; K02435; AAA30685.1; -.

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Blood coagulation, Glycoprotein, Serine protease;
Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
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CAAF6833F894C209 CRC64;
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GAMMA-CARBOXYGLUTAMIC A
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CHARGE RELAY SYSTEM.
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BY SIMILARITY.
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PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01019; EGF_CA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS000114; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
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                                         InterPro; IPR001881; EGF_Ca.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
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SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; 1.
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EGF-like.
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80.96%
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Pfam; PF00089; trypsin; 1.
Pfam; PF00594; gla; 1.
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        HSSP; P04070; 1PCU.
PIR; A00928; KXBO
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PROSITE; PS01186;
PROSITE; PS01187;
                MEROPS; S01.218;
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AACTTCATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATG 1014
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   Mismatches:
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                                                                     US-09-763-153-1 (1-1245) x PRTC_BOVIN (1-456)
                                  Gaps:
 71.81%
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   Best Local Similarity:
                  Query Match:
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-1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-1- PTM; THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
-1- MINGELLANDOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECCGNITION OF THE
1015 GTGTCTGAGAACATGCTGTGTGCGGGCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGC 1074
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                                                                     GACAGTGGGGGGCCCATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTG 1134
                                                                                        SerTrpGlyGluGlyCysGlyArgLeuTyrAsnTyrGlyValTyrThrLysValSerArg 435
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).
                                                                                                                                                                                                                 TACCTCGACTGGATCCATGGGCACATCAGAGACAAGGAAGCCCCC 1239
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MEDLINE-92329550; PubMed=1627650;
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PIR; S24312; S24312.
HSSP; P04070; 1PCU.
MEROPS; S01.218; -.
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61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
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Conservative:
Mismatches:
Indels:
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        461 AA; 51912 MW;
                                               2.14e-80
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PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS01187; EGF_1; 1.

PROSITE; PS01187; EGF_2; 2.

PROSITE; PS00011; GLU_CARBOXYLATION; 1.

PROSITE; PS000134; TRYPSIN_LDOM; 1.

PROSITE; PS00135; TRYPSIN_LDOM; 1.

PROSITE; PS00135; TRYPSIN_LSER; 1.

PROSITE; PS00135; TRYPSIN_LSER; 1.

PROSITE; PS00136; TRYPSIN_LSER; 1.

PROFILIKE domain; Repeat; Endothelial cell; Hydrolase; Signal.

FFT SIGNAL

BY SIMILARITY.

BY SIGNAL

BY SIMILARITY.

PROPEP 33 41 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
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PROTEIN C HEAVY CHAIN (BY SIMILARITY).
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(POTENTIAL).
(POTENTIAL).
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
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GAMMA-CARBOXYGLUTAMIC ACID
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(BY SIMILARTOW)
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GAMMA-CARBOXYGLUTAMIC ACID
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SERINE PROTEASE.
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                                                           InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; Vitk_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF00594; gla; 1.
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                  Chymotrypsin.
EGF-like.
Asx_hydroxyl
                                                                                                                                                     PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_like; 1.
SMART; SM00005; GLA; 1.
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InterPro; IPRO01314;
InterPro; IPRO00561;
                                            InterPro; IPR001881;
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-!- SUBUNT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENEXME IS THEN ACTIVATED BY THROMEIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS FRACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Nucleotide structure and characterization of the murine gene encoding anticoagulant protein C.";
                                                                                                                                                                                                         Br. J. Haematol. 86:590-600(1994).
-I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
                                            955 AACTTCATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATG 1014
                                                                                                                         1015 GTGTCTGAGAACATGCTGTGTGCGGGCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGC 1074
                                                                                                                                                                                                                                                                                         135 AGCTGGGGTGAGGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGC 1194
341 GlyTrpGlyTyrGlnSerAspLysValLysAspGlyArgArgArgArgArhrPheIleLeu 360
                                                                                                                                                361 ThrPheIleArgIleProLeuAlaAlaArgAsnAspCysMetGlnValMetAsnAsnVal 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y., "A comparative study of partial primary structures of the catalytic region of mammalian protein C."; Br. J. Haematol. 86:590-600(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P33587; 035498;
01-FBB-1994 (Rel. 28, Last sequence update)
11-FBB-1994 (Rel. 128, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jalbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T., "Isolation and characterization of a mouse protein C cDNA."; J. Biochem. 111:491-495(1992).
                                                                                                                                                                                                                                                                                                                                                                  1195 TACCTCGACTGGATCCATGGGCACATCAGAGGAGGAAGCCCCCCAGAAG 1245
                                                                                                                                                                                                                                                                                                                                                                                                        441 TyrLeuLysTrpIleHisSerTyrIleGlyGluArgAspValSerLeuLys 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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MEDLINE=94318474; PubMed=8043441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/SvJ;
MEDLINE=98152576; PubMed=9493582;
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SEQUENCE OF 274-434 FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSU01.55; raircomm.com; Serine protease; Blood coagulation; Glycoprotein; Serine protease; Gamma-carboxyjutamic acid; Calcium-binding; Vitamin K; Hydroxylation; Gamma-carboxyjutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
-i- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
-i- PTM: THE VITAMIN K-DEPENDENT, ENGYMATIC CARBOXYLATION OF SOME
GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
-i- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN C LIGHT CHAIN (BY SIMILARITY).
PROPEIN C HEAVY CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
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                                                                        SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
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SERINE PROTEASE.
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BY SIMILARITY
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PROSITE: PS01082; EGF_1; 1.
PROSITE: PS01187; EGF_2; 2.
PROSITE: PS01187; EGF_CA; 1.
PROSITE: PS00011; GLU_GARBOXYLATION; 1.
PROSITE: PS00134; TRYPSIN_LOS; 1.
PROSITE: PS00134; TRYPSIN_HIS; 1.
PROSITE: PS00135; TRYPSIN_HIS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR001881; EGF_Ca.
Interpro; IPR0012383; GLA_blood.
Interpro; IPR001254; Ser_protease_Try.
Interpro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                  HSSP, P04070; 1PCU.
MEROPS; S01.218; -.
MGD; MG197771; Proc.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001314; ChymotryPsin.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                      EMBL; D10445; BAA01235.1; -.
EMBL; AF034569; AAC33795.1; -.
EMBL; D43755; BAA07812.1; -.
PIR; JX0210; JX0210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00008; EGF; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
Pfam; PF00594; gla; 1.
PRINTS; PR00722; CHYMOTRYESIN.
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_like; 1.
SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp_SPc; 1.
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                                                                       HYDROXYLATION (BY SIMILARITY). CHARGE RELAY SYSTEM.
                                                                                                                               BY SIMILARITY.
N'LINKED (GICNAC. ...) (POTEN N'LINKED (GICNAC. ...) (POTEN N'LINKED) (GICNAC. ...)
                                    (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
GAMMA-CARBOXYGLUTAMIC ACID
                        GAMMA-CARBOXYGLUTAMIC ACID
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Conservative:
Mismatches:
                                                              (BY SIMILARITY)
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CHARGE RELAY
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1075 GACAGTGGGGGCCCCATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTG 1134
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MEDLINE-94318474; PubMed=8043441;
MEDLINE-94318474; PubMed=8043441;
Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic region of mammalian protein C.";
Br. J. Haematol. 86:590-600(1994).
-I- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
201 AspLeuGluAspGluLeuGluProAspProArgIleValAsnGlyThrLeuThrLysGln 220
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
15-UNN-2002 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment).
                                                                   GGAGACAGCCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGGTGGGCCTGCGGGGCA
                                                                                                                                  GTGCTCATCCACCCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAG
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1195 TACCTCGACTGGATCCATGGGCACATCAGAGACAAG 1230
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                                                                                                                                                                                                                                                     994 AGCGAGGTCATGAGCAACATGGTGTCTGAGAACATGCTGTGTGCGGGCATCCTCGGGGAC 1053
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                                 -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           874 GGCCAGGAGACCCTCGTGACGGGCTGGGGCTACCACAGCAGCCGAGAGAAGGAGGAGCCAAG
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N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                Blood coagulation; Glycoprotein; Serine protease; Hydrolase. NON_TER
                                                                    -!- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27D78F185B2FCC69 CRC64;
                  THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
                                                                                       -!- SIMILARITY; BELONGS TO PEPTIDASE FAMILY S1.
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Indels:
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                Interpro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
SMART; SM0020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; 1.
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835.00
98.14%
95.65%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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1114 TGGTTCCTGGTGGCCCTGGTGAGCTGGGGCTGTGGGCTCCTTCACAACTACGGC 1173
                                                                                                                                                                                                                                                                                                               Eukaryotā; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001881; EGF_Ca.
Interpro; IPR0012883; GIA_blood.
Interpro; IPR001254; Ser_protease_Try.
Interpro; IPR000294; Vitk_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=97256311; Pubmed=9101642;
                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
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PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_like; 1.
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Pfam; PF00089; trypsin; 1.
                                                                                                                                 STANDARD;
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                                                     1174 GTT 1176
                                                                              161 Val 161
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InterPro;
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SMART; SM00069; GLA; 1.

R SMART; SM00020; Tryp_SPC; 1.

R PROSITE; PS000120; ASX_HINDROXIL; 1.

R PROSITE; PS001022; EGF_1; 1.

R PROSITE; PS01186; EGF_2; 2.

R PROSITE; PS01187; EGF_CARBOXILATION; 1.

R PROSITE; PS00134; TRYPSIN_DOM; 1.

R PROSITE; PS00134; TRYPSIN_DOM; 1.

R PROSITE; PS00135; TRYPSIN_LHS; 1.

R PROSITE; PS00135; TRYPSIN_LHS; 1.

R Glamma-carboxyglutamic acid; Hydrolase; Serine protease; Plasma; Blood coagulation; M Gamma-carboxyglutamic acid; Hydrolase; Serine protease; Plasma; Blood coagulation; Signal; Zymogen; EGF-like domain; Repeat.

SIGNAL 1 20 POTENTIAL.

CHAIN 41 180 FACTOR X LIGHT CHAIN.
                                                                                                                                                                  ACTIVATION PEPTIDE.
ACTIVATED FACTOR XA, HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                             HYDROXYLATIY).

CHARGE RELAY SYSTEM.

BY SIMILARITY.

N-LINKED (GICNAC. ...) (POTENTIAL).

N-LINKED (GICNAC. ...) (POTENTIAL).

N-LINKED (GICNAC. ...) (POTENTIAL).
                                                                                                                                                                                                       SERINE PROTEASE.
GAMMA-CARBOXYGLUTAMIC ACID (BY
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GAMMA-CARBOXYGLUTAMIC ACID (BY
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FACTOR X HEAVY CHAIN.
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        SQ
        SEQUENCE
        490 AA;
        53965 MW;
        3A39FA85AF2A6D11 CRC64;

        Alignment Scores:
        2.88e-36
        Length:
        490

        Pred. No.:
        2.88e-36
        Length:
        490

        Score:
        814.50
        Matches:
        173

        Percent Similarity:
        33.71%
        Conservative:
        66

        Best Local Similarity:
        38.8%
        Mismatches:
        159

        Query Match:
        1.98*
        Indels:
        47

        DB:
        1
        Gaps:
        9
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121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 TGTGGGAGG------CCCTGGAAGCGGATGGAGAAGAAGCGCAGTCAC---- 462
                                                                                       61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
                                                                                                     361 GCGCCTGGCTACAAGCTGGGGGACGTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT 420
                                                                                                                                                                                                                                                                                                                                                                                                                     152 AlaserGlyTyrThrLeuGlyAspAsnGlyLysSerCysIleSerThrGluLeuPhePro 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 AsnGluGluAsnGluGlyPheCysGlyGlyThrIleLeuSerGluTyrHisValLeuThr 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             865 AATCAGGCCGGCCAGGAGCCCTCGTGACGGGCTGGGGCTACCACAGAGAGGAGAAG 924
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                                                                                                                                                              241 CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGGGAGGTGAGCTTCCTCAATTGCTCGCTG
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                                                                                                                                                                        1165 AACTACGGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATCCATGGGCACATCAGA 1224
                         985 AATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCTGAGAACATGCTGTGTGCGGGCATC 1044
                                                                                                                                       426 ArgAspThrTyrPheValThrGlyIleValSerTrpGlyGluGlyCysAlaArgLysGly 445
                                                                                                                                                                                     MEDILINE-94062825; PubMed-8243461;
Inoue K., Morita T.,
"Identification of 0-linked oligosaccharide chains in the activation
peptides of blood coagulation factor X. The role of the carbohydrate
moleties in the activation of factor X.";
  367 GluMetGlyArgLeuSerThr---ThrLeuLySMetLeuGluValProTyrValAspArg 385
                                                386 AsnSerCysLysArgSerSerSerPheThrIleThrGlnAsnMetPheCysAlaGlyTyr 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               [1] MEDLINE-84247315; PubMed=6330671; MEDLINE-84247315; PubMed=6330671; Fung M.R., Campbell R.M., McGillivray R.T.A.; Fung M.R., Campbell R.M., McGillivray R.T.A.; "Blood coagulation factor X mRNA encodes a single polypeptide chain "Blood coagulation factor Sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Amino acid sequence of the light chain of bovine factor X1 (Stuart
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-76053069; PubMed-1059093;
Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine factor X1 (Stuart factor): amino-acid sequence of heavey
                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
13-MG-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MCMILLEN B.A., Fujikawa K., Kisiel W.; "The occurrence of beta-hydroxyaspartic acid in the vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
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                                                                                                                                                                                                                                                                                                 492 AA.
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-1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.
--- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then Arg-1-Ile bonds in prothrombin to form thrombin.
--- SUBGNUTT: THE THO CHALMS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
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*Activation of bovine factor X (Stuart factor): conversion of factor Xa-alpha to factor Xa-beta.";
Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
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MEDLINE-96387194; PubMed-8794734;
Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
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Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
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Eur. J. Biochem. 218:153-163(1993).
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Biochemistry 11:4899-4903(1972).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation; Gamma-carboxyglutanic acid; Hydroxylation; Calcium-binding; Vitamin K; Signal; Zymogen; BGF-like domain; Repeat; Sulfation; 3D-structure. I 23 POTEWIAL.
                                                                          PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY). OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY). MINCELLANDOUGS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLOMAIN. SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI. SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
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EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL)
EGF-LIKE 2.
SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAY BE REMOVED BUT IS NOT NECESSARY FOR
               PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATED FACTOR XA, HEAVY CHAIN.
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GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
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CHARGE RELAY SYSTEM.
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Pfam; PF00008; trypsin; 1.
Pfam; PF00008; trypsin; 1.
Pfam; PF00001; dlas; 1.
PRINTS; PR00722; CHNOTRYPSIN.
PRINTS; PR00722; CLABLOOD.
SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_Like; 1.
SMART; SM00000; EGF_Like; 1.
PROSITE; PS00010; ASX_HVDROXYL; 1.
PROSITE; PS001010; ASX_HVDROXYL; 1.
PROSITE; PS01186; EGF_L; 1.
PROSITE; PS01186; EGF_L; 1.
PROSITE; PS01187; TRYPSIN DOM; 1.
                                                                                                                                                                                                                                                                                                                   EMBL, X00673; CAA25286.1; -
PIR; A00925; EXBO.
PDB; 1APO; 31-JAN-94.
PDB; 1UWE; 15-MAY-94.
PDB; 1WHE; 15-MAY-97.
MEROPS; S01.216, -
GlyCoSuiteDB; P00743; -
InterPro; IPR001514; CHymotrypsin.
InterPro; IPR001514; CHymotrypsin.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR000561; EGF-20.
InterPro; IPR000581; GCF_20.
InterPro; IPR002383; GLA_blood.
InterPro; IPR00254; Ser_protease_Try.
InterPro; IPR00254; Ser_protease_Try.
InterPro; IPR00254; VitK_dep_GLA.
                                                                PTM: N- AND O-GLYCOSYLATED
 DISULFIDE BONDS
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Mismatches:
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TISSUE-Liver;

Ruiz S.R., Blajchman M.A., Clarke B.J.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM: FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROFEDLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR XTO FACTOR XA BY LIMITED PROFEDLYSIS: FACTOR VIIA MILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
                                                                                                                                                                                                                                                                                                                                               970 CCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCTGAGAACATG 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            422 HisValThrArgPheLysAspThrTyrPheValThrGlyIleValSerTrpGlyGluGly 441
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382 ProTyrValAspArgSerThrCysLysLeuSerSerSerPheThrIleThrProAsnMet 401
                                                                                                                                                                                                                                                                                                  365 -----ArgThrHisGluLysGlyArgLeuSerSerThrLeuLysMetLeuGluVal 381
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P98139; P79224;
01-FEB-1996 (Rel. 33, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 PheCysAlaGlyTyrAspThrGlnProGluAspAlaCysGlnGlyAspSerGlyGlyPro
                                                                                                                                                              GAGCGCGAGCTCAATCAGGCCGGCCAGGAGACC---CTCGTGACGGGCTGGGGCTACCAC
                                                                                                                                                                                                                                                       910 AGCAGCCGAGAGAGGAGGCCAAGAGAACCGCACCTTCGTCCTCAACTTCAAGATT
                                                                     793 CAGCCGGCCACCCTCTCGCAGACCATAGTGCCCATCTGCCTCCCGGACAGCGGCCTTGCA
                                                                                                                329 ThrProIleArgPheArgArgAsnValAlaProAlaCysLeuProGluLysAspTrpAla
                                                                                                                                                                                                         349 GluAlaThrLeu-----MetThrGlnLysThrGlyIleValSerGlyPheGly----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Res. Suppl. 69:231-238(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93190306; PubMed=8383365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conversion accelerator).
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
EGF-like domain; Repeat; Signal; Hydroxylation.
SIGNAL 1 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FACTOR IXA, OR THROMBIN) (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstative European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 2.
CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
              form factor Xa.
SUBGUIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULETDE BOWD (BY SIMILARITY).
TISSUE SPECIFICITY: PLASMA.
                                                                   -!- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLEAVAGE (BY FACTOR XA, FACTOR XIIA,
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BY SIMILARITY.
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                                                                                              CALCIUM (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                             InterPro; IPR000561; BGF-1ike.
InterPro; IPR000742; BGF_2.
InterPro; IPR001881; BGF_Ca.
InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; Vitk_dep_GLA.
Pfam; PF000089; EGF; 2.
Pfam; PF000089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE: PS00010; ASX HYPROXIL; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
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                                                                                                                                                                                                                                                                                                                 Chymotrypsin.
EGF-like.
                                                                                                                                                                                                                                                                                                   Asx_hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00134; TRYPSIN_HIS; 1 PROSITE; PS00135; TRYPSIN_SER; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00594; gla; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                           EMBL; U77477; AAB37326.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF_like; 1.
GLA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tryp_SPc; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_like;
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InterPro; IPR001314;
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SMART; SM00020;
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172 TyrProCysGlyLysVal---ProAlaLeuGluLysArgGlyAla-------- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 ------SerAsnProGlnGlyArglleValGlyGlyLysValCysProLys 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535 GGAGACAGCCCTGGCAGGTGGTCCTGGACTCAAAGAAGAAGCTGGCCTGCGGGGCA 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 AGCTGTGCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 LeualaAspPhedluGlyArgAsnCysGluLysAsnLysAsnAspGlnLeuIleCysMet 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AGCCIGIGCIGCGGGACGGGACGTGCAICGACGGCAICGGCAGCITCAGCIGCGACTGC 240
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                                                                                                                                                                                                                                      HYDROALLATION (ST. N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-ITUKED (GLCNAC. . .) (POTENTIAL).
                                        GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                             .LINKED (GLCNAC. . .) (PC
                                                                                                                                                                                                                                                                                                                                                                               Conservative:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 GluGlnSerGluHisLysProGlySerProGluValThrGlyAsnMetPheCysAlaGly 370
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                                                                                                                                                                                                                                                                                                                                                                                                                          886 CTCGTGACGGGCTGGGGC-----TACCACAGCAGCGAGAGAAGGAGGCCAAGAGA 936
                                                                                                                                                       260 GlnValArgHisValAlaGlnLeulleMetProAspLysTyrValProGlyLysThrAsp 279
                                                                                                                                                                                                              766 AATGACATGGCAGTGCAGCCTGGCCCAGCCCGCCACCTCTCGCAGACCATAGTGCCC 825
                                                                                                                                                                                                                                                               280 HisaspilealaLeuLeuargLeuLeuGlnProAlaAlaLeuThrAsnAsnValValPro 299
                                                                                                                                                                                                                                                                                                                  300 LeuCysLeuProGluArgAsnPheSerGluSerThrLeuAlaThrlle---ArgPheSer 318
                                                                                                       706 CIGGACCIGGACAICAAGGAGGICIICGICCACCCCAACIACAGCAAGAGCACCACCGAC 765
646 TCCAAGAAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGGCGCTGGGAGAAGTGGGAG 705
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01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
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MEDLINE-91065352; PubMed-2174359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Virus activating protease) (VAP).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstationuse by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
           "An endoprotease homologous to the blood clotting factor X as a determinant of viral tropism in chick embryo.";

EMBO '9 :4189-4195(1990).

-! FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrompin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.
-! FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENDAI VIRUS, NDV, STIE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLANTOIC
                                                                                                                                                                                                    -I- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR WAS BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
                                                                                                                                                                                                                                                                                                                                   -!- FTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FACTOR X LIGHT CHAIN.
FACTOR X HEAVY CHAIN.
ACTIVATION PEPTIDE.
ACTIVATED FACTOR XA, HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-!-Thr and then
                                                                                                                                                                                                                                                MORE DISULEIDE BOODS.
-1-TISSUE SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE.
-1-PTM: THE VITAMIN K-DEPRNDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OR 30, OR 31 (POTENTIAL).
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PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS001011; GLU_CARBOXVLATION; 1.
PROSITE; PS00240; TRYPSIN_LOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
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InterPro; IPR000294; Vitk_dep_GLA.
Pfam; PP00008; BGF; 2.
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InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR001681; EGF-2.
InterPro; IPR001881; EGF-C.
InterPro; IPR001438; EGF-II.
InterPro; IPR001438; EGF-II.
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113 LeuAspGlyTyrGlnGlyLysAsnCysGluPheValIlePro---LysTyrCysLysIle 131
                                            GACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGC----- 351
                                                                                      132 AsnAsnGlyAspCysGluGlnPheCysSerIleLysLysSerValGlnLysAspValVal 151
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MEDLINE-91216473; PubMed-1902434;
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"Cloning and expression in COS-1 cells of a full-length cDNA encoding
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                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 13-488 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coagulation factor X: evidence for identification of residue 63 beta-hydroxyaspartic acid."; Biochemistry 22:2875-2884(1983).
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Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochemistry 25:5098-5102(1986).
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                                                                                                                               Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                              **RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.

**MEDLINE-98283982; PubMed-9618463;

**MEDLINE-98283982; PubMed-9618463;

**MEDLINE-98283982; PubMed-9618463;

**Amata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;

**Taructural basis for chemical inhibition of human blood coagulation

**La Proc. Natl. Acad. Sci. U.S.A. 95:6830-6635(1998).

**C -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.

**C -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Thr and then Arg-1-ILe bonds in prothrombin to form thrombin.

**Arg-1-ILe bonds in prothrombin to form thrombin.

**INDINIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR BY TWO ARG RESIDUES AND ARE HELD TOGETHER BY I OR WARD INTERTEDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PTM: N- AND O-GLYCOSYLATED.
-!- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
MEDLINE-93360277; PubMed-8355279; Padmanabhan K., Park C.H., Bode W., Budmanabhan K.P., Tulinsky A., Park C.H., Bode W., Huber R., Blankenship D.T., Cardin A.D., Kisiel W.; "Structure of human des(1.45) factor Xa at 2.2-A resolution."; J., Mol. Biol. 232:947-966(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
-!- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; K03194; AAA52450...;

; K03194; AAA52451.1;

;i, L29433; AAA52764.1; -...

BL; L00390; AAA52764.1; JOINED.

AA52764.1; JOINED.

*AA52764.1; JOINED.
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InterPro; IPR000561; BGF-11ke.
InterPro; IPR00142; BGF_2.
InterPro; IPR001881; BGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; K03194; AAA52490.1; -.
encoding human factor X.";
Gene 84:517-519(1989).
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K01886; AAA52486.1; -
M33297; AAA52636.1; -
A00924; EXHU.
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AAA52764.1;
AAA52764.1;
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PIR; A25853; A25853.
PIR; A24478.
PDB; 1HCG; 08-MAY-95.
PDB; 1FAX; 29-CCT-97.
PDB; 1FXX; 17-JUN-98.
PDB; 1XXA; 23-MAR-99.
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Genew; HGNC:3528; F10.
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MEROPS; S01.216; -.
GlycoSuiteDB; P00742;
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Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation; Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K; Signal; Zymogen; EGF-like domain; Repeat; 3D-structure.
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EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 2.
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N-LINKED (GLCNAC. .).
/FTIG-CAR_000013.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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O-LINKED (GALNAC...).
N-LINKED (GLCNAC...).
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GAMMA-CARBOXYGLUTAMIC
GAMMA-CARBOXYGLUTAMIC
                                                                                                                                                                                                                                                                                                                        FACTOR X LIGHT CHAIN. FACTOR X HEAVY CHAIN.
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Mismatches:
Indels:
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                                                                                              SMART; SMO0179; EGF_CA; 1.
SMART; SMO0101; EGF_LIKe; 1.
SMART; SMO0001; EGF_LIKe; 1.
SMART; SMO00001; EGF_LIKe; 1.
SMART; SMO00001; TYP_SPC; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_2; 2.
PROSITE; PS01011; EUL_CARBOXYLATION; 1.
PROSITE; PS00113; EGF_CA; 1.
PROSITE; PS00134; TRYPSIN, IS; 1.
PROSITE; PS00134; TRYPSIN, IS; 1.
PROSITE; PS00135; TRYPSIN, IS; 1.
InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; Vitk_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF00594; gla; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
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1090 ATGGTCGCCTCCTTCCACGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGAGGGC 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Amino acid sequence and posttranslational modifications of human factor VIIa from plasma and transfected baby hamster kidney cells."; Biochemistry 27:7785-7793(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T., Pedersen A.H., Hedner U.;
                                                                                  403 PheCysAlaGlyTyrAspThrLysGlnGluAspAlaCysGlnGlyAspSerGlyGlyPro 422
                                                                                                                                                                                                                                                                                                                                                                                                                                 FA7_HUMAN STANDARD; PRT; 466 AA.
P08709; 014339;
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (Eptacog alfa).
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MEDLINE-87260948; PubMed=3037537;
O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
O'Hagen F.S., Murray M.J.;
Nucleotide sequence of the gene coding for human factor VII, a
Nucleotide sequence of the gene ricipating in blood coagulation.";
Vitamin K-dependent protein participating in blood coagulation.";
Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANTS THR-352; GLN-413 AND LYS-445. Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.; submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C., Woodbury, R.G., Hart C.E., Insley M.Y., Kisiel W., Kurachi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of a cDNA coding for human factor VII.";
Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
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                                                                                                                                                                                                                                                                                                                  463 AspargSerMetLysThrargGlyLeuProLys 473
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MEDLINE=86205965; PubMed=3486420;
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Alignment Scores:
Pred. No.:
                                                                                                                                        Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.; "A new trisaccharide sugar chain linked to a serine residue in the first EGF-like domain of clotting factors VII and IX and protein Z."; Adv. Exp. Med. Biol. 281:121-131(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE-22340074; PubMed=1634227;
Marchetti G., Patracchini P., Gemmati D., Derosa V., Pinotti M.,
Rodorigo G., Casonato A., Girolami A., Bernardi F.;
"Detection of two missense mutations and characterization of a repeat
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99126538; PubMed-9925787;
Zhang E., St Charles R., Tulinsky A.;
"Structure of extracellular tissue factor complexed with factor VIIa
(Xy12-Glc) O-glycosidically linked to a serine residue in the first epidermal growth factor-like domain of human factors VII and IX and protein Z and bovine protein Z.";

J. Biol. Chem. 264:20320-20325(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J., Meade T.W., Tuddenham E.G.D.;
"Purification and characterization of factor VII 304-Gln: a variant molecule with reduced activity isolated from a clinically unaffected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS CHARLOTTE GLN-139 AND GLN-212.
MEDLINE=94264305; PubMed=8204879;
Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
Roberts H.R., Blajchman M., Monroe D.M., High K.A.;
                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF-
MEDLINE-96175641; PubMed-8598903;
                                                                                                                                                                                                                                                                                                                                                                                              CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
                                                                                                                                                                                                                                                                             Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A., Konigsberg W.H., Nemreson Y., Kirchhofer D.; "The crystal structure of the complex of blood coagulation factor VIIa with soluble tissue factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Solution structure of the N-terminal EGF-like domain from human factor VII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takamiya O., Kemball-Cook G., Marin D.M.A., Cooper D.N., von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H., Tuddenham E.G.D., McVey J.H.; "Detection of missense mutations by single-strand conformational polymorphism (SSCP) analysis in five dysfunctional variants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marchetti G., Ferrati M., Patracchini P., Redaelli R., Bernardi "A missense mutation (178cys-->Tyr) and two neutral dimorphisms (115His and 33Ser) in the human coagulation factor VII gene.", Hum. Mol. Genet. 2:1055-1056 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J., Drakenberg T.;
                                                                                                   STRUCTURE OF CARBOHYDRATE ON SER-112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibited with a BPTI mutant.";
J. Mol. Biol. 285:2089-2104(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry 37:10605-10615(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hum. Mol. Genet. 2:1355-1359(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 105-145.
MEDLINE-98367502; Pubmed=9692950;
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                                                                                                                   MEDLINE~91344709; PubMed=2129367
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                                                                                                                                                                                                                                                                                                                                                           Nature 380:41-46(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blood 78:132-140(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT GLN-364.
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MEDLINE=95072589; PubMed=7981691;
Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
Brodeghiero F., Marchetti G.;
"Topoclogically equivalent mutations causing dysfunctional coagulation factors VII (294Ala-->Val) and X (334Ser-->Pro).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hum. Mutat. Suppl. 1:5189-5191(1998).

-1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMEIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR VIOLATION. CALCIUM.
    "Severe factor VII deficiency caused by mutations abolishing the cleavage site for activation and altering binding to tissue factor."; Blood 83:3524-3535(1994).
                                                                                                                                                                                                                                                                                                         "Factor VII Mie: homozygous asymptomatic type I deficiency caused by an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is a common, probably ancient mutation causing factor VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97001216; PubMed=8844208;
Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
Lunghi B., Rodeghiero F., Marchetti G.;
"Mutation pattern in clinically asymptomatic coagulation factor VII
                                                                                                                                                                                                                                                                                                                                                                                                                                          Arbini A.A., Mannucci P.M., Bauer K.A.,
"A Thr359Met mutation in factor VII of a patient with a hereditary
deficiency causes defective secretion of the molecule.";
Blood 87:5085-5094(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: PLASMA.
PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98112461; PubMed-9452082;
Alshimavi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;
"Two new missense mutations (P134T and A244V) in the coagulation
factor VII gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N., Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M., Zalzov R., Seligsohn U.;
"Ala244Val is a common, probably ancient mutation causing factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
                                                                                                                                                                                                                                                 MEDLINE-95064662; PubMed-7974346;
Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS W-283; K-325; V-358; Q-364; E-402 AND Q-413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deficiency in Moroccan and Iranian Jews.";
Thromb. Haemost. 76:283-291(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS MALTA THR-194 AND VAL-304.
                                                                                                                                                                                                                                                                                                                                              catalytic domain.";
Thromb. Haemost. 71:773-777(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96247510; PubMed=8652821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT VAL-304.
MEDLINE=97037613; PubMed=8883260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutat. 8:108-115(1996).
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                                                                                                                                                                                                                                   VARIANT MIE HIS-307
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                                                                            VARIANT VAL-354
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-!- PHARMACEUTICAL: Available under the names Niastase or Novoseven (Novo Nordisk). Used for the treatment of bleeding episodes in

DISEASE: DEFECTS IN F7 CAN CAUSE COAGULOPATHY.

466

Length:

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946 TICGICCICAACTICATCAAGATICCCGIGGICCCGCACAAIGAGIGCAGGCGAGGICAIG 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      886 CTCGTGACGGCCTGGGGCTACCACAGCAGAGAAAGAAGGAGGCCAAGAGAAACCGCACC 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    706 CIGGACCIGGACATCAAGGAGGICTICGICCACCCCAACTACAGCAAGAGCACCACCGAC 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 GlnSerArgArgValAlaGlnValIleIleProSerThrTyrValProGlyThrThrAsn 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  766 AATGACATCGCACTGCTGCTGCCCCAGCCCGCCACCTCTCGCAGACCATAGTGCCC 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ThrieulleAsnThrIleTrpValValSerAlaAlaHisCysPheAspLysIleLysAsn 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            652 -----AAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGGCGCTGGGAAATGGAA 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         595 GIGCICAICCACCCCCCCCGGGIGCIGACAGGGGCCCCACIGCAIGGAIGAGICCAAG--- 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        535 GGAGACAGCCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGCTGGCCTGCGGGGCA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475 ACAGAAGACCAAGAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 ------SerLysProGlnGlyArglleValGlyGlyLysValCysProLys 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 AGCIGIGCGCCTGGCTACAAGCIGGGGGACGACCICCIGCAGTGICACCCCGCAGTGAAG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 ArgcysHisGludlyTyrSerLeuLeuAlaAspGlyValSerCysThrProThrValGlu 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 TTCCCTTGTGGGGGCCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGAC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 SerProCysGlnAsnGlyGlySerCysLysAspGlnLeuGlnSerTyrIleCysPheCys 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 LeuproAlaPheGluGlyArgAsnCysGluThrHisLysAspAspGlnLeuIleCysVal 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 CIGGACAACGGCGGCTGCACGCAITACIGCCIAGAGGAGGTGGGCTGGCGGCGC---IGI 354
                                                                                                                                                                                                                                                                                                                                                              121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                   181 AGCCTGTGCCTGCCGGCACGGCACGTGCATCGGCATCGGCAGCTTCAGCTGCGACTGC 240
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                                                                                                                                                                                                                                                                     61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
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                                                                                                                                                                               1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACCAGCCTGGAGCGGGAGTGCATAGAGGAG
                                                                                                                                                                                                                                                                                              193 TyrProCysGlyLys---IleProIleLeuGluLysArgAsnAla----
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                   Conservative:
Mismatches:
Matches:
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MEDLINE=9144709; PubMed=2129367;
MEDLINE=914709; PubMed=2129367;
Medianga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
Twanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
Advaraga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
Advaraga S., Nishimura H., Karabata S., Kisiel W., Hase S., Ikenaka S., Ikanaka S., Ik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89213999; PubMed=3149637;
Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;
"A new trisaccharide sugar chain linked to a serine residue in bovine blood coagulation factors VII and IX.";
J. Blochem. 104:867-868(1988).
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                                                                                                                                                                                       1051 GACCGGCAGGATGCCTGCGAGGGCGACAGTGGGGGGCCCATGGTCGCCTCCTTCCACGGC 1110
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                                                                          1006 ------ACCAACATGGTGTCTCTGAGAACATGCTGTGTGCGGGCATCCTCGGG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                             395 GlySerLysAspSerCysLysGlyAspSerGlyGlyProHisAlaThrHisTyrArgGly 414
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||| ::: :::||| ::: 374 ||| 355 LeuGluLeuMetValLeuAsnValProArgLeuMetThrGlnAspCysLeuGlnGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 19, Last sequence update)
(Rel. 41, Last annotation update)
factor VII (EC 3.4.21.21) (Serum prothrombin conversion
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-!- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T., Iwanaga S.; Bovine factor VII. Its purification and complete amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE OF CARBOHYDRATE ON SER-52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 263:14868-14877(1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1231 GAAGCCCCC 1239
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PROSITE; PS00134; TRYPSIN_LIS; 1.
PROSITE; PS00134; TRYPSIN_LIS; 1.
Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; CGF-like domain; Repeat.

CHAIN 1 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
BGF-LIKE 2.
SERINE PROTEASE.
CLEAVAGE (BY FACTOR XA, FACTOR XIIA,
  GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAMMA-CARBOXYGLUTAMIC ACID.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SUBSTRATE (BY SIMILARITY).
BY SIMILARITY.
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N-LINKED (GLCNAC. ..).
                                               -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
PIR; A31979; A31979.
-- SIRSP: P08709; 1BF9.
-- MEROPS; S01.215; -- .
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                                                                                                                                                             R InterPro; IPR000152; Asx, hydroxyl.
R InterPro; IPR0001514; Chymotrypsin.
InterPro; IPR0001314; Chymotrypsin.
InterPro; IPR000141; EGF_1ike.
InterPro; IPR001811; EGF_2.
R InterPro; IPR001811; EGF_2.
R InterPro; IPR001814; EGF_II.
R InterPro; IPR001284; EGF_II.
R InterPro; IPR001284; EGF_II.
R InterPro; IPR0001284; EGF_II.
R Fam; PF00008; EGF_2.
R Fam; PF00008; EGF_2.
R Fam; PF00008; EGF_1I.
R FRINTS; PR00010; EGF_ELOOD.
R PRINTS; PR00010; EGF_ELOOD.
SMART; SM00010; EGF_CA; I.
SMART; SM00010; EGF_LA; I.
SMART; SM00001; EGF_LA; I.
SMART; SM00010; EGF_II.
R PROSITE; PS00010; ASX_HYDROXYL; I.
PROSITE; PS01010; ASX_HYDROXYL; I.
PROSITE; PS01018; EGF_2; 2.
PROSITE; PS01018; EGF_CA; I.
PROSITE; PS010144; ADAPONTE; INDOM; I.
PROSITE; PS010144; ADAPONTE; INDOM; I.
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                                                                                                                                                              1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCCTGGAGCGGGAGTGCATAGAGGAG 60
                                                                                                                                                                                                                                                                                                                                                                241 CGCAGCGCCTGGCAGGCCCGCTTCTGCCAGCGCGAG---GTGAGCTTCCTCAATTGCTCG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                1 AlaAsnGlyPheLeuGluGluLeuLeuProGlySerLeuGluArgGluCysArgGluGlu 20
                                                                                                                                                                                                                                                                               298 CTGGACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGC----TGGCGGCGCTGT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 AGCIGIGCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415 TTCCTTGTGGGAGGCCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGAC 474
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133 TyrProCysGlyLys---IleProValLeuGluLysArgAsnGly------- 146
                                                                                                                                                                                                                                                                                                                                                                                475 ACAGAAGACCAAGAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 ------SerLysProGlnGlyArgileValGlyGlyHisValCysProLys 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    535 GGAGACAGCCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGAAGCTGGCCTGCGGGGCA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    595 GIGCICATCCACCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAG--- 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 ArgGlyAsnLeuThrAlaValLeuGlyGluHisAspLeuSerArgValGluGlyProGlu 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       652 -----AAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGGCGGGGAGAAGTGGGAG 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        706 CTGGACCTGGACATCAAGGAGGTCTTCGTCCACCCCAACTACAGCAAGAAGCACCACCGAC 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 GlnGluArgArgValAlaGlnIleIleValProLysGlnTyrValProGlyGlnThrAsp 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          766 AATGACATCGCACTGCACCTGGCCCAGCCCGCCACCCTCTCGCAGACCATAGTGCCC 825
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407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;
                                                                                Conservative:
Mismatches:
                                                                   Matches:
                                                        Length:
                                                                                                        Indels:
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                                                                                                                                    US-09-763-153-1 (1-1245) x FA7_BOVIN (1-407)
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54.898
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Best Local Similarity:
Query Match:
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97127167; PubMed-8972017;
Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
Idusogie E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
"Nucleotide structure and characterization of the murine blood
coagulation factor VII gene.";
Thromb. Haemost. 76:957-964(1996).

1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIA, FACTOR IXA, OR
AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X
BY LIMITED PROTEOLYSIS. FACTOR VIIA THEN CONVERTE FACTOR XA
FRACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
                                                                                                                                                                                                                                                                                                                                                                                                                           1111 ACCTGGTTCCTGGTGGGCCTGGGTGAGGTGAGGGCTGTGGGGCTCCTTCACAACTAC 1170
                                                                                                                                                                                                                                                                                                                   1051 GACCGGCAGGATGCCTGCGAGGGCGACAGTGGGGGGGCCCATGGTCGCCTCCTTCCACGGC 1110
                                                                                                                                                                                                            1006 AGCAAC-----ATGGTGTCTGAGAACATGCTGTGTGCGGCATCCTCGGG 1050
                                                                                                       946 ITCGTCCTCAACTTCATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGGTCATG 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: Hydrolyzes one Arg-1-11e bond in factor X to
                                                                                                                                                                                                                                                                                                                                               ||| ::: ::||| :::
297 -----LeuMetValValLeuValProArgLeuThrGlnAspCysLeuGlnGlnSer 314
                                                                                                                                                                                                                                                              315 ArgGlnArgProGlyGlyProValValThrAspAsnMetPheCysAlaGlyTyrSerAsp 334
                                         886 CICGIGACGGGCIGGGGCIACCACAGCAGCCGAGAGAGGAGGCCAAGAGAAACCGCACC 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBGNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).
-1- TISSUE SPECIFICITY: PLASMA.
-1- PTH: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1171 GGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATCCAT------GGGCAC 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CALCIUM (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       446 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conversion accelerator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P08709; 1BF9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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P70375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F7 OR CF7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FA7 MOUSE
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Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLEAVAGE (BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN) (BY.SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL). EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYDROXYLATION (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAMMA-CARBOXYGLUTAMIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAMMA-CARBOXYGLUTAMIC ACID.
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GAMMA-CARBOXYGLUTAMIC ACID.
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GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FACTOR VII LIGHT CHAIN. FACTOR VII HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-like domain; Repeat; Signal; Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FACTOR IXA, OF
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO1011; GLU_CARBOXYLATION; 1. PROSITE; PS50240; TRYPSIN_DOM; 1. PROSITE; PS0134; TRYPSIN_HIS; 1. PROSITE; PS0135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLA-RICH.
                                                                                           Interpro; IPR000742; EGF_2.
Interpro; IPR001881; EGF_Ca.
Interpro; IPR002383; GIA_blood.
Interpro; IPR001254; Ser_protease_Try.
Interpro; IPR000294; VitK_dep_GIA.
                                                                                                                                                                                                                                                       PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
SMART; SM00179; EGF_CA; 1.
SWART; SM00001; EGF_Ike; 1.
SWART; SM000001; EGF_Ike; 1.
PROSITE; PS00010; ASX_HYDROXIL; 1.
PROSITE; PS01186; EGF_2; FALSE_NEG.
PROSITE; PS01186; EGF_2; FALSE_NEG.
MEROPS; S01.215; -.
MGD; MGI:109325; F7.
Interpro; IPR000152; GAx_bydroxyl.
Interpro; IPR001314; Chymotrypsin.
Interpro; IPR000561; EGE-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50276 MW;
                                                                                                                                                                                                  Pfam; PF00008; EGF; 2.
Pfam; PF00089; trypsin; 1.
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Length:

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61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
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                                                                                                                                                     1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCCTGGAGCGGGAGTGCATAGAGGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 TyrprocysGlyArg---IleProValValGluLysArgAsnSerSerArgGlnGly 192
                                                                                                                                                                                           42 AlaAsnSerLeuLeuGluGluLeuTrpProGlySerLeuGluArgGluCysAsnGluGlu 61
                                                                                                                                                                                                                                                                       62 GlnCysSerPheGluGluAlaArgGluIlePheLysSerProGluArgThrLysGlnPhe 81
                                                                                                                                                                                                                                                                                                                                       415 TTCCCTTGTGGGAGGCCCTGGAAGCGGATGGAGAAGAAGGAGCAGTCACCTGAAACGAGAC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475 ACAGAAGACCAAGAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGG 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          535 GGAGACACCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGGTGGCCTGCGGGGCA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          946 ITCGICCICAACTICAICAAGAITCCCGIGGICCCGCACAAIGAGIGCAGCGAGGICAIG 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 GlyGluCysProTrpGlnAlaVal --- LeuLysIleAsnGlyLeuLeuLeuCysGlyAla 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      595 GIGCTCATCCACCCTCCTGGGTGCTGACAGGGGCCCACTGCATGGATGAGTCCAAG--- 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               652 -----AAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGGCGGCGGGAGAAGTGGGAG 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 TrpGlyAsnileThrValValMetGlyGluHisAspPheSerGluLysAspGlyAspGlu 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  706 CTGGACCTGGACATCAAGGAGGTCTTCGTCCACCCCAACTACAGCAAGAAGACCACCGAC 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 GlnValArgArgValThrGlnValIleMetProAspLysTyrIleArgGlyLysIleAsn 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                766 AATGACATGGCACTGCTGCACCTGGCCCAGCCGCCACCCTCTGGCAGACCATAGTGCCC 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 LeucysLeuProGluLysSerPheSerGluAsnThrLeuAlaArgIle---ArgPheSer 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 ArgvalSerGlyTrpGlyGlnLeuLeuAspArgGlyAlaThrAla------ 335
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                       71
                       Conservative:
Mismatches:
      Matches:
                                                                 Indels:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                    1051 GACCGGCAGGATGCCTGCGAGGGGGGCGACATGGTCGTCGTCGTCGTCCTTCCACGGC 1110
                                                                                                                                                                                       1111 ACCTGGTTCCTGGTGGGCCTGGTGAGCTGGGGCTGTGGGCTCTTCACAACTAC 1170
                                                                                                                                                                                                                                                           1171 GGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATCCATGGGCACATCAGAGACAAG 1230
356 LysHisSerSerAsnThrProLyslieThrGluAsnMetPheCysAlaGlyTyrMetAsp 375
                                                                                                                                         376 GlyThrLysAspAlaCysLySGlyAspSerGlyGlyProHisAlaThrHisTyrHisGly 395
                                                                                                                                                                                                            Axelrod J.H., Read M.S., Brinkhous K.M., Verma I.M.; "Phenotypic correction of factor IX deficiency in skin fibroblasts of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 86:10095-10099(1989).
-!- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IONS, PHOSPHOLIPIDS, AND FACTOR VIIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES THE
                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD TOGETHER BY ONE OR MORE DISULFIDE BONDS.

DISEASE: HEWOPHILIA B IS DUE TO DEFECTS IN FACTOR IX.

MISCELLANEOUS: CALCIUM BINDS TO THE GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-90099303; PubMed-2461310; Evans J.P., Brinkhous K.M., Brayer G.D., Reisner H.M., High K.A.; "Canine hemophilia B resulting from a point mutation with unusual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLA) RESIDUES AND, WITH STRONGER AFFINITY, TO ANOTHER SITE, BEYOND THE GLA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Evans J.P., Watzke H.H., Ware J.L., Stafford D.W., High K.A.;
"Molecular cloning of a CDNA encoding canine factor IX.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 87:5173-5177(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                          452 AA.
                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90311364; PubMed=2367529;
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                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT HEMOPHILIA B GLU-418
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blood 74:207-212(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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15-JUN-2002
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P19540;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-sib.ch).
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CLEAVAGE (BY FACTOR XIA) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATION PEPTIDE.
FACTOR IXA (ACTIVE FORM) HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 2.
                                                                                                                                                                                                   DR InterPro; IPR0000561; EGF-11ke.

InterPro; IPR0001881; EGF_Ca.

InterPro; IPR0012383; GLA_blood.

InterPro; IPR001254; Ser_Protease_Try.

InterPro; IPR001254; Ser_Protease_Try.

Rean; Pr000089; EGF; 2.

Rean; Pr000089; LYPSAIN; 1.

REAN; PR000089; LYPSAIN; 1.

REAN; PR000015 GLABILOOD.

REAN; SM00072; CHYMOTRYPSIN.

REANT; SM00072; CHYMOTRYPSIN.

REANT; SM00019; EGF_CA; 1.

REANT; SM00020; EGF_L; 1.

REANT; SM00020; EGF_L; 1.

REANT; SM00020; EGF_L; 1.

REANT; SM0010; ASX HYPROXYL; 1.

REANT; PR0011; GLG_CARBOXYLATION; 1.

REANT; PR0011; GLG_CARBOXYLATION; 1.

REASTE; PS00013; TRYPSIN_HIS; 1.

REASTE; PS00013; TRYPSIN_LRS; 1.

REASTE; PS00134; TRYPSIN_LRS; 1.

REASTE; PS00134; TRYPSIN_LRS; 1.

REASTE; PS00135; TRYPSIN_LRS; 1.

REASTE; PS0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FACTOR IXA (ACTIVE FORM) LIGHT CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY). HYDROXYLATION (BY SIMILARITY).
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GAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
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GAMMA-CARBOXYGLUTAMIC ACID
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946 TTCGTCCTCAACTTCATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGGGGAGGTCATG 1005
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670 GGAGAGIAIGACCIGCGCGCTGGGAGAAGTGGGAGCIGGACCIGGACAICAAGGAGGTC 729
                                 271 GlygluHisAsnThrGluLysArgGluHisThrGluGlnLysArgAsnValIleArgThr 290
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).
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MEDLINE=85190593; PubMed=3857619;
MEDLINE=85190593; PubMed=3857619;
MCGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,
Graham J.B., Stafford D.W.;
"Evidence for a prevalent_dimorphism in the activation peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-84236100; PubMed-6329734;
Anson D.S., Choo K.H., Rees D.J.G., Giannelli F., Gould K.G.,
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Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).
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Jaye M., dela Salle H., Schamber F., Balland A., Kohli V., Findeli A., Tolstoshev P., Lecocq J.P.; "Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-base synthetic oligonucleotide probe deduced from the amino acid sequence of bovine factor IX."; "Nucleic Acids Res. 11:2325-2335(1983).
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MEDLINE-86189947; PubMed=3009023;
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MEDLINE-78194509; Pubmed-659613;
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MEDLINE-88127096; PubMed=3340835;
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MEDLINE-90078229; PubMed=2592373;
                                                                                       MEDLINE=83220788; PubMed=6687940;
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Huddleston J.A., Brownlee G.G.;
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               "The gene structure of huma
EMBO J. 3:1053-1060(1984).
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Biochemistry 36:2132-2138(1997).
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                                                                                                610 TCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTTGTCAGGCTT
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Manmalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Sarkar G., Koeberl D.D., Sommer S.S.,
"Direct sequencing of the activation peptide and the catalytic domain
Genomics 6:133-143(1990).
                                                  -1- FUNCTION: FACTOR IX IS A VITAMIN K-DEPENDENT PLASMA PROTEIN THAT PARTICIPATES IN THE INTRINSIC PATHWAY OF BLOOD COAGULATION BY CONVERTING FACTOR X TO ITS ACTIVE FORM IN THE PRESENCE OF CA++ IONS, PHOSPHOLIPIDS, AND FACTOR VIIIA.
                                                                                                                       form factor xa.
-!- SUBUNIT: FACTOR IX IS ACTIVATED BY FACTOR XIA, WHICH EXCISES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLEAVAGE (BY FACTOR XIA) (BY SIMILARITY).
CLEAVAGE (BY FACTOR XIA) (BY SIMILARITY).
                                                                                                                                               ACTIVATION PEPTIDE AND THUS PRODUCES A MOLECULE CONSISTING OF 2 CHAINS HELD FOGETHER BY ONE OR MORE DISULEIDE BONDS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FACTOR IXA (ACTIVE FORM) HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; EGF_1; 1.
; EGF_2; 2.
; EGF_CA; 1.
; GLU_CARBOXXLATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; Vitk_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00594; 91a; 1.
SMART; SW00179; EGF_CA; 1.
SMART; SW00069; GLA; 1.
SWART; SW00020; Tryp_SPC; 1.
PROSITE; PS00110; ASX_HYDROXYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00134; TRYPSIN_HIS; 1. PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRYPSIN_DOM;
                                                                                                                                                                                                                                                                                                                            EMBL; M23109; AAA37629.1; -.
EMBL; M26236; AAA37630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00008; EGF; 2.
Pfam; PF00089; trypsin; 1.
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                                                                                                                                                                                                                                                                                                                                                         PIR; JQ0419; JQ0419.
HSSP; P00740; ICFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001881;
                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S01.214; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01187;
PROSITE; PS00011;
PROSITE; PS50240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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(BY SIMILARITY).

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430 CCC-----TGGAAGCGGATG 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 GluGlyArgAsnCysGluLeuAspAlaThr-----CysAsnIleLysAsnGlyArg 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 CysLysGlnPheCysLysAsnSerProAspAsnLysValIleCysSerCysThrGluGly 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 TACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCTTGTGGGAGG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 TyrGlnLeuAlaGluAspGlnLysSerCysGluProThrValProPheProCysGlyArg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTCTGGTCCAAGCAC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GICGACGGIGACCAGIGCIIGGICIIGCCCIIGGAGCACCCGIGCGCCAGCCIGIGCIGC 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 AsnGlyGlyIleCysLysAspAspIleSerSerTyrGluCysTrpCysGlnValGlyPhe 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 CIGGAGGAGCICCGICACAGCAGCCIGGAGCGGGAGIGCAIAGAGGAGAICIGIGACIIC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluglualaargGluValPheGluAsnThrGluLysThrThrGluPheTrpLysGlnTyr 79
                                                                                                                                                                                                                        BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-INKED (GLCNAC. . .) (POTENTIAL).
N-INKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                            HYDROXYLATION (BY SIMILARITY).
                                                                                                                                             (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
GAMMA-CARBOXYGLUTAMIC ACID
                     GAMMA-CARBOXYGLUTAMIC ACID
                                (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
                                                                GAMMA-CARBOXYGLUTAMIC ACID
                                                                                   GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                  (BY SIMILARITY).
GAMMA-CARBOXYGLUTAMIC ACID
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-> I (IN REF. 2).
EF439C840D6CBC1A CRC64;
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CHARGE RELAY SYSTEM.
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Mismatches:
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                                                       (BY SIMILARITY)
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Matches:
                                                                             SIMILARITY)
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726.00
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1036 GCGGGCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGCGACAGTGGGGGGGCCCATGGTC 1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 ThrGluValGluGlyThrSerPheLeuThrGlyIleIleSerTrpGlyGluGluCySAla 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Coagulation factor X (EC 3.4.21.6) (Trocarin prothrombin activator). Tropldechis carinatus (Australian rough-scaled snake).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Lepidosauria, Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Notechinae; Tropldechis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 TyrvalThrProlleCys------valalaAsnArgGluTyrThrAsnIle 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343 PheLeuLysPheGlySerGly-----TyrValSerGlyTrpGlyLysValPheAsn 359
                                                                                                                                                                                                                                                                                                                         640 GATGAGTCCAAGAAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGGCGCTGGGAAAG 699
                                                                                                                                                                                                                                                                                                                                             268 LysProGlyAspLysIleGluValValAlaGlyGluTyrAsnIleAspLysCluAsp 287
                                                                                                                                                                                                                                                                                                                                                                                               100 TGGGAGCTGGACCTGGACATCAAGGAGGTCTTCGTCCACCCCAACTACAGCAAGAGCACC 759
                                                                                                                                                                                                                                                                                                                                                                                                                              288 ThrGluGlnArgArgAsnVallleArgThrIleProHisHisGlnTyrAsnAlaThrIle 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 ASDLySTyrSerHisAspIleAlaLeuLeuGluLeuAspLysProLeuIleLeuAsDSer 327
                                               462
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|169 AlaSerIleSerTyrSerSerLysLysIleThrArgAlaGluThrValPheSerAsnMet 188
                                                                              189 AspTyrGluAsnSerThrGluAlaValPheIleGlnAspAspIleThrAspGlyAlaIle 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            916 CGAGAGAAGGAGGCCAAGAGAAACCGCACCTTCGTCCTCAACTTCATCAAGATTCCCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395 AlaGlyTyrArgGluGlyGlyLysAspSerCysGluGlyAspSerGlyGlyProHisVal
                                                                                                                                                                                   520 AAGATGACCAGGCGGGGAGACAGCCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAG
                                                                                                                                                                                                      580 CIGGCCIGCGGGGCAGIGCICAICCACCCCICCIGGGIGCIGACAGCGGCCCACIGCAIG
                                                                                                                                                                                                                                                                         463 CIGAAACGAGACACAGAAGACCAAGAAGACCAAGIAGAI----CCGCGGCICAIIGAIGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1156 CICCTICACAACTACGGCGITTACACCAAAGTCAGCCGCTACCTCGACTGGATC 1209
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NR SMART; SM00101; GEGELA; 1.

SMART; SM0001; GEGELA; 1.

SMART; SM00001; GEGELA; 1.

SMART; SM00001; GEGELA; 1.

NR SMART; SM000001; GEGELA; 1.

NR SMART; SM000001; GEGELA; 1.

NR PROSITE; PS000010; ASX HYDROXYL; 1.

NR PROSITE; PS00101; GEGELA; 1.

NR PROSITE; PS001013; TRYPSIN_LOM; 1.

NR PROSITE; PS001013; TRYPSIN_LOM; 1.

NR GALYCOPFOLGEIG; HYDROLAGE; 1.

NR GALYCOPPOLGEIG; HYDROLAGE; 1.

KW GALYCOPPOLGEIG; HYDROLAGE; SETINE PROCEDURATION; M. GARMAR-CARDOXYGILURALIC CALGIUM-DINGING; VITAMIN K; M. CALGIUM-DINGING; VITAMIN K;
                                          MEDLINE=99326314; PubMed=10397729;
Joseph J.S., Chung M.C.M., Jeyaseelan K., Kini R.M.;
"Amino acid sequence of trocarin, a prothrombin activator from
Tropidechis carinatus venom: its structural similarity to coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
-!- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                           in venom.

--- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-Ile bonds in prothrombin to form thrombin.

--- SUBBUNIT: THE THO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR AND ARE HELD TOGETHER BY I OR MORE DISULFIDE BONDS.

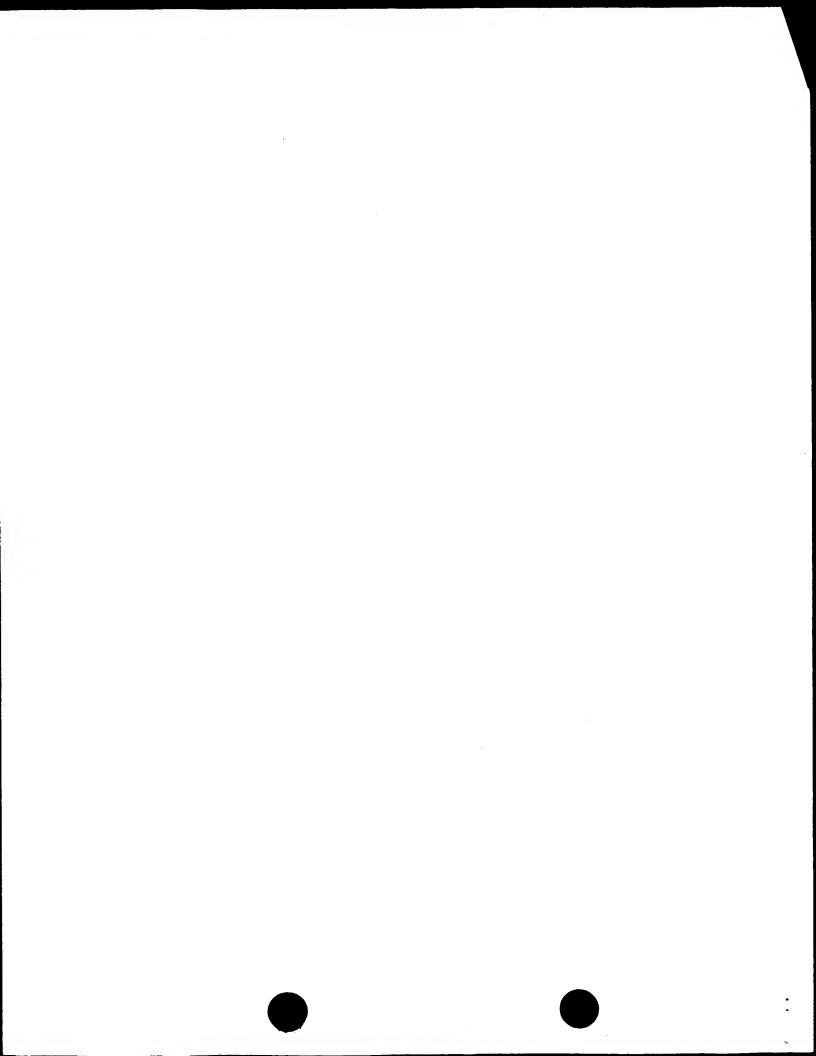
--- PTW: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
                                                                                                                                                                                                 FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that Converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting. Acts as a toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAMMA-CARBOXYGLUTAMIC ACID.
GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACTOR X HEAVY CHAIN.
ACTIVATED FACTOR XA, HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACTOR X LIGHT CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR000152; Asx.hydroxyl.
InterPro: IPR0001314; Chymotrypsin.
InterPro: IPR0001314; Chymotrypsin.
InterPro: IPR000742; EGF_11ke.
InterPro: IPR001481; EGF_Ca.
InterPro: IPR001488; EGF_II.
InterPro: IPR001283; GLA_blood.
InterPro: IPR001254; Ser_Protease_Try.
InterPro: IPR0002294; Vitk_dep_GLA.
PRINTS; PR000722; CHYMOTRPSIN.
PRINTS; PR00012
SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zymogen; EGF-like domain; Repea
                                                                                                                                                 factor xa.";
Blood 94:621-631(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALCIUM
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61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
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N-LINKED (GLCNAC.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        985 AATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCTGAGAACATGCTGTGTGCGGGCATC 1044
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                      295 HisThrCysMetLeuSerSerAspPheArgIleThrGlnAsnMetPheCysAlaGlyTyr 314
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"A comparative study of partial primary structures of the catalytic
region of mammalian protein C.";
Br. J. Haematol. 86:590-600(1994).
-!- FUNCTION: PROTEIN C. IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 ArgAspThrHisPhelleThrGlyIleIleSerTrpGlyGluGlyCysAlaArgLysGly 354
                                                                                                                                                                        805 CTCTCGCAGACCATAGTGCCCATCTGCCTCCGGACAGCGGCCTTGCAGAGCGCGAGCTC 864
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
Vitamin-K dependent protein C (EC 3.4.21.69) (Autoprothrombin IIA)
(Aniicoagulant protein C (Blood coagulation factor XIV) (Fragment).
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                                                                                                                                                                                              ---AGCAAGAGCACCGACGACATGACATCGCACTGCTGCACCTGGCCCAGCCCGCCACC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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721 AAGGAGGTCTTCGTCCAC---
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994 AGCGAGGTCATGAGCAACATGGTGTCTGAGAACATGCTGTGTGCGGGCATCCTCGGGGAC 1053
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                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                    Blood coagulation; Glycoprotein; Serine protease; Hydrolase
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                                               InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN_SER; 1.
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717.00
86.96%
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30.68%
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Search completed: March 17, 2003, 17:32:35 Job time : 57 secs



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  PRELIMINARY;
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Q=/CG901_1(YGPPO_SPOO_IVG9)763153/runat_11032003_084247_1993/app_query.fasta_1.1415

Q=/CG901_1(YGPPO_SPOO_IVG9)763153/runat_11032003_084247_1993/app_query.fasta_1.1415

Q=CG901_1(YGPPO_SPOO_IVG9)763153/runat_1 = WIP=rIN=blosum62 -TRANS=human40.cdi

-LOSPENT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi

-LIST=60 -DOCALIGN=200 -THR_SCORE=EDCT -THR_MAN=0 -ALIGN=20

-USER=USO9763153_6CGN_1 - 186_4cunat_11032003_084247_11993 -NCPU=6 -CCPU=3

-NOA_ELEXT - NO_MANP - LARGEQUERY - NGC_SCORES=0 -WAIT -LONGIGG - DEV_TIMEOUT=120

-WARN_INEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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   (without alignments)
   6980.372 Million cell updates/sec
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            GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                      protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                                671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 60 summaries
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sp_invertebrate:*
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121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
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                                                                                               Brenig B.; -- "Molecular characterization and chromosomal assignment of the canine
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Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;
"Analysis of canine protein C gene polymorphisms.";
Anim. Genet. 30:237-238(1999).
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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SMART; SM00069; GLA; 1.

SMART; SM00069; GLA; 1.

R PROSITE; PS00010; ASX, HYDROXIL; 1.

R PROSITE; PS00012; EGE_1; UNKNOWN_1.

R PROSITE; PS01186; EGE_CA; 2.

R PROSITE; PS01186; EGE_CA; 3.

R PROSITE; PS0011; GLU_CARBOXYLATION; 1.

R PROSITE; PS00134; TRYPSIN_LSR; 1.

R PROSITE; PS00135; TRYPSIN_LSR; 1.
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PROTEIN C LIGHT CHAIN.
PROTEIN C CONNECTING DIPEPTIDE.
PROTEIN C HEAVY CHAIN.
7AD3A8C1C34E59FF CRC64;
                                                                                  Leeb T., Kopp T., Deppe A., Breen M., Matis U., Brunnberg
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Matches:
Conservative:
Mismatches:
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InterPro; 1PR00152; Asx_hydroxyl.
InterPro; 1PR001514; Chymotrypsin.
InterPro; 1PR001814; EdF_Ca.
InterPro; 1PR001881; EdF_Ca.
InterPro; 1PR001284; Ser_Protease_Try.
InterPro; 1PR000284; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN,
PRINTS; PR00001; GLABLOOD.
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                                                                                                                                                 Mamm. Genome 10:135-139(1999).
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Query Match:
                                  NCBI_TaxID=9615;
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AGCCTGTGCTGCGGGGACGCACGTGCATCGACGGCATCGGCAGCTTCAGCTGCGACTGC
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61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCCGGGAGGGGGAGTGCATAGAGGAG 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the EMBL/GenBank/DDBJ databases
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Last annotation update)
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Matches:
Conservative:
Mismatches:
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InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; Vitk_dep_GLA.
Pfam; PF00008; EGF; 2.
                                                                                                                                                                            Created)
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                                                                                    PRT;
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1631.00
83.74%
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                                                                                                                                                               (TrEMBLrel. 19, (TrEMBLrel. 19, 1; (TrEMBLrel. 21, 1
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Submitted (SEP-2001) to the
EMBL; BC013896; AAH13896.1;
                                                                                        PRELIMINARY;
                                                                                                                                                               01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                        01-DEC-2001 (TrEMBLre) 01-JUN-2002 (TrEMBLre) Similar to protein C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l; Proc.
                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LISSUE-LIVER
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                                                                                                                         Q91WN8;
                                                                                    Q91WN8
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RESULT 2
                                          Q91WN8
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361 GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT 420
                                                                       1135 AGCTGGGGTGAGGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGC 1194
                                                      421 TGTGGGAGGCCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGACACAGAA 480
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201 AspLeuGluAspGluLeuGluProAspProArgIleValAsnGlyThrLeuThrLysGln 220
                                                                                                                                                                                                                                      360 ThrPheIleArgIleProLeuValAlaArgAsnGluCysValGluValMetLysAsnVal 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 AlaProGlyTyrGluLeuAlaAspAspHisMetArgCysLysSerThrValAsnPhePro 181
                                                                                                            481 GACCAAGAAGACCAAGTA-----GATCCGCGGCTCATTGATGGGAAGATGACCAGGCGG 534
                                                                                                                                                                                                                      595 GIGCICAICCACCCCICCIGGGIGCIGACAGGGGCCCACIGCAIGGAIGAGICCAAGAAG 654
                                                                                                                                                                                                                                                                             655 CTCCTTGTCAGGCTTGGAGAGTATGACCTGCGGCGTGGGAGAAGTGGGAGCTGGACCTG 714
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBL_raxID-10090;
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181 AGCCTGTGCGGGCACGCCACGTGCATCGACGCATCGGCAGCTTCAGCTGCGACTGC 240
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                                                       "Complete sequence of UC72A01.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                        SMART: SM00020; Tryp_SPC; 1.

PROSITE: PS00010: ASX_HYDROXXL; 1.

PROSITE: PS001023: EGF_2; 2.

PROSITE: PS01186: EGF_2; 2.

PROSITE: PS01181: EGF_CA: TRYPSIN_LINE

PROSITE: PS00101; GLU_CARBOXYLATION; 1.

PROSITE: PS0011; GLU_CARBOXYLATION; 1.

PROSITE: PS00134; TRYPSIN_LINE; DOM; 1.

PROSITE: PS00134; TRYPSIN_LINE; 1.

Calcium-binding: EGF_like domain: Glycoprotein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0293BC25E9D3ED16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                 MGD; MGI:97771; Proc.
InterPro; IPR00152; Asx_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001381; GEF_11ke.
InterPro; IPR001381; GEF_0a.
InterPro; IPR001294; GLA_blood.
InterPro; IPR001294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00701; GLABLCOD.
SMART; SM00101; GLABLCOD.
SMART; SM00001; GLABLCOD.
SMART; SM00001; GLABLCOD.
SMART; SM00001; GLABLCOD.
SMART; SM00001; GLABLCOD.
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1625.00
83.50%
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HSSP; P04070; 1PCU.
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Best Local Similarity:
                SEQUENCE FROM N.A.
                                                                                                                                                       MEROPS; S01.218;
                             STRAIN-C57BL;
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Pred. No.:
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955 AACTICATCAAGATICCCGTGGICCCGCACAAIGAGTGCAGCGAGGTCAIGAGCAACAIG 1014
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                                                  421 TGTGGGAGGCCCTGGAAGCGGATGGAGAAGAAGCGCCAGTCACCTGAAACGAGACACAGAA 480
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                         361 GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT
                535 GGAGACAGCCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGCTGGCCTGCGGGGCA
                                                                                                                                                                                                                595 GIGCICAICCACCCCICCIGGGIGCIGACAGCGGCCCCACTGCAIGGAIGAGTCCAAGAAG
                                                                                                                                                                                                                              241 ValLeuileHisThrSerTrpValLeuThrAlaAlaHisCysValGluGlyThrLysLys
                                                                                                                                                                                                                                                                      655 CICCITGICAGGCITGGAGAGIATGACCIGCGGCGCIGGGAGAAGIGGGAGCIGGACCIG
                                                                                                                                                                                                                                                                                              261 LeuThrValArgLeuGlyGluTyrAspLeuArgArgArgAspHisTrpGluLeuAspLeu
                                                                                                                                                                                                                                                                                                                          715 GACATCAAGGAGGTCTTCGTCCACCCCAACTACAGCAAGAGCACCACCGACAATGACATC
                                                                                                                                                                                                                                                                                                                                                                                                                               895 GGCTGGGGCTACCACAGCAGCAGAGAAGAAGGAGCCAAGAAAACCGCACCTTCGTCCTC
                                                                                                        481 GACCAAGAAGACCAAGTA----GATCCGCGCTCATTGATGGGAAGATGACCAGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1195 TACCTCGACTGGATCCATGGGCACATCAGAGACAAG 1230
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NCBI\_TaxID=10116;

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STRAIN-SPRAGUE-DAWLEY,
MEDLINE=96093365, PubMed-8578539,
Stanton C., Ross R.P., Hutson S., Wallin R.;
Stanton Corpetition between vitamin K-dependent clotting factors for intracellular processing by the vitamin K-dependent gamma-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thromb. Res. 80:63-73(1995).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
EMBL; X79807; CAR56202.1; -.
HSSP; P00742; LXKA.
MEROPS; S01.216; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AGCCTGTGCGGGCACGCACGTGCATCGACGCCATCGGCAGCTTCAGCTGCGACTGC
                                                                                                                                                                                                                                              InterPro; IPRO01312; ASA_INGLOXY.

InterPro; IPRO01312; Chymotrypsin.

InterPro; IPR000361; EGF-1ike.

InterPro; IPR000361; EGF-2.

InterPro; IPR001381; GIA_blood.

InterPro; IPR001284; Ser_Protease_Try.

InterPro; IPR001284; VitK_dep_GLA.

InterPro; IPR001294; VitK_dep_GLA.

InterPro; IPR001294; VitK_dep_GLA.

R Pfam; PF000089; LTypsin; 1.

R Pfam; PF000089; LTypsin; 1.

R RRINTS; PR000179; EGF_CA; 1.

R SMART; SM00001; GLABLOOD.

R SMART; SM00001; GLAS_II.

R SMART; SM00001; GLA: 1.

R SMART; SM00001; GGF_1ike; 1.

R SMART; SM00186; EGF_2; 1.

R PROSITE; PS001186; EGF_2; 1.

R PROSITE; PS01186; EGF_2; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01148; TRYPSIN_BR; 1.

R PROSITE; PS01148; TRYPSIN_BR; 1.

R PROSITE; PS0114; EGF_CA; 1.
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1165
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Matches:
Conservative:
Mismatches:
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482 AA; 54265 MW; 02846781
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                                                                                                                                                                                                                                   InterPro; IPR000152; Asx_hydroxyl InterPro; IPR001314; Chymotrypsin
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818.50
54.71%
37.00%
35.02%
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est Local Similarity:
uery Match:
               SEQUENCE FROM N.A.
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                                                                                                                 carboxylase."
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1102 TICCACGGCACCIGGTICCIGGIGGGCCIGGIGAGCIGGGGIGAGGCCIGIGGGCTCCTT 1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               404
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                                       132 AspAsnGlyAspCysAspGlnPheCysArgGluGluGlnAsnSerValValCysSerCys 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTTGTCAGGCTTGGAGAGTATGACCTG 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 AlaAlaHisCysLeuHisGlnAlaLysArgPheLysValArgValGlyAspLeuAsnThr 291
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                                                                                                                                                                    ------CGCAGTCACCTG
                                                                                                                                                                                                                                                                                     252 AspGluGluThrAspGlyPheCysGlyGlyThrIleLeuAsnGluPheTyrIleLeuThr
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                                                                                  GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT
                                                                                                                                                                                                            172 CysGlyLysThrAsnLysGlyArgAlaLysArgSerValAlaLeuAsnThrSerAsnSer
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                                                                                                                                                                                                                                                                                                                                                                                  212 SerGluLeuLeuAsnLeuAsnLysThrGluProGluAlaAsnSerAspAspValIleArg
                                                                                                                                                                                                                                                      466 AAACGAGACACAGAAGACCAAGAAGACCAAGTAGAT----
                                                                                                                                                                    TGTGGGAGGCCCTGGAAGCGGATGGAGAAGAAG
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RESULT 5

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MEDLINE-9834793; Pubmed-96849791; Liang Z., Cooper A., DeFord M.E., Carmeliet P., Collen D., Lastellino F.J., Rosen E.D.; Cartellino F.J., Rosen E.D.; Edstelling and characterization of a cDNA encoding murine coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00010; TYP, SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01022; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01011; GIU_CARBOXYLATION; 1.
PROSITE; PS00101; TRYPSIN_DOM; 1.
PROSITE; PS001134; TRYPSIN_HIS; UNKNOWN_1.
PROSITE; PS001135; TRYPSIN_HIS; UNKNOWN_1.
CALCIUM-binding; EGF_like domain; Glycoprotein; Hydrolase; Repeat;
                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                        Cooper A., Liang Z., Castellino F.J., Rosen E.D.; "Cloning and Characterization of the Murine Factor X Gene."; Thromb. Haemost. 0:0-0(2000).
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILX S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COAGULATION FACTOR X.
8AC09DE5EF9D271E CRC64;
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162
77
158
48
                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
Indels:
                 481 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROFY, FOOVAZ, JANA.
MEROFY, SOL.216; -..
MCD. MGI:103107, FIO.
InterPro; IPR000152; ASx_hydroxyl.
InterPro; IPR001314; Chymctrypsin.
InterPro; IPR000151; BGF-1; InterPro; IPR00142; BGF-2.
InterPro; IPR001881; BGF-2.
InterPro; IPR001881; BGF-2.
InterPro; IPR001881; BGF-2.
InterPro; IPR001881; BGF-2.
InterPro; IPR000184; VitK_dep_GLA.
Pfam; PF000089; BGF; 2.
Pfam; PF000089; trypsin; 1.
PRINTS; PR007021; CHYMOTRYPSIN.
PRINTS; PR007021; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                 PRT;
                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL6 X CBA; TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                Thromb. Haemost. 80:87-91(1998).
                                                                                       Coagulation factor X precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF211347; AAC36345.1; -. EMBL; AF211347; AAF22980.1; -.
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SWART; SW00001; EGF_11ke; 1.
SWART; SW00069; GLA; 1.
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53.718
36.408
33.988
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               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P00742; 1XKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00069;
SMART; SM00020;
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                                                                                                                                                                                                                                                                                                                                            STRAIN-129SJ
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              088947
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088947
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465
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                                                                                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                              301 GACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGCGCTGTAGCTGT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                             172 CysGlyLysIleThrThrGlyArgArgLysArgSerValAlaLeuAsnThrSerAspSer 191
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192 GluLeuAspLeuGluAspAlaLeuLeuAspGluAspPheLeuSerProThrGluAsnPro 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    508 CTCATTGATGGGAAGATGACCAGGCGGGGAGACAGCCCCTGGCAGGTGGTCCTGCTGGAC 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 LysGluGluGlyAsnGluMetValHisGluValAspValValIleLysHisAsnLysPhe 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               925 GAGGCCAAGAGAAACCGCACCTTCGTCCTCAACTTCAAGATTCCCGTGGTCCCGCAC 984
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                                 1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCCTGGAGCGGGGAGTGCATAGAGGAG 60
                                                    181 AGCCTGTGCTGCGGGCACGGCACGTGCATCGACGGCATCGGCAGCTTCAGCTGCGACTGC
                                                                                                                                                                                                                                                                                              241 CGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 TGTGGGAGGCCCTGGAAGCGGATGGAGAAGAAG-------CGCAGTCACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      466 AAACGAGACACAGAAGAC-----CAAGAAGACCAAGTAGATCCG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      568 TCAAAGAAGAAGCTGGCCTGCGGGGCAGTGCTCATCCACCCCTCCTGGGTGCTGACAGCG
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US-09-763-153-1 (1-1245) x 088947 (1-481)
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1165 AACTACGGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATCCATGGGCACATCAGA 1224
985 AATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCTGAGAACATGCTGTGTGCGGGCATC 1044
                                                405 GluAlaLysLeuGluAspAlaCysGlnGlyAspSerGlyGlyProHisValThrArgPhe 424
              445 LysTyrGlylleTyrThrLysValThrThrPheLeuLysTrplleAspArgSerMetLys 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning and recombinant expression of mouse coagulation factor X."; Thromb. Res. 92:33-41(1998).
                                                                                                                                                                                                                                                                                                                                                                           Plasmid pBluescript.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Coagulation factor X precursor (EC 3.4.21.6).
                                                                                                                                                                                                                                                                             481 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
SMART; SW00179; EGF_CA: 1.
SMART; SW00001; EGF_Like; 1.
SMART; SW00069; GLA: 1.
SMART; SW00069; GLA: 1.
SMART; SW00009; ASX_HYDROXYL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01011; EGF_CA: 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS00013; TRYPSIN_DOW; 1.
PROSITE; PS00134; TRYPSIN_HS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_HS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98454993; PubMed=9783672;
Heidtmann H.H., Kontermann R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRYPSIN FAMILY.
EMBL; AJ222677; CAA10933.1; -.
                                                                                                                                                                                                 1225 GACAAGGAAGCCCCC 1239
                                                                                                                                                                                                                        465 AlaArgValGlyPro 469
                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      LISSUE=LIVER
                                                                                                                                                                                                                                                                                                               01-JUN-1998
01-JUN-2002
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95 -----CysGlnAsnGlnGlyAlaCysArgAspGlyIleGlyGlyTyrThrCysThrCys 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
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192 GluLeuaspLeuGluAspAlaLeuLeuAspGluAspPheLeuSerProThrGluAsnPro 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 CysGlyLysIleThrThrGlyArgArgLysArgSerValAlaLeuAsnThrSerAspSer 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            568 TCAAAGAAGAAGCTGGCCTGCGGGGCAGTGCTCATCCACCCCTCCTGGGTGCTGACAGCG 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 GluAspAsnGluGlyPheCysGlyGlyThrIleLeuAsnGluPheTyrIleLeuThrAla 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  628 GCCCACTGCATGGATGAGTCCAAGAAGCTCCTTGTCAGGCTTGGAGGAGTATGACCTGCGG 687
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                                                                                                                                                                                                                                                                                                               1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCCTGGAGCGGGAGTGCATAGAGGGA 60
Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Plasmid; Repeat; Serine protease; Signal. SIGNAL 1 40 POTENTIAL.
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                                                      CF702DE5EF9D97AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
                                                                                                                            Length:
Matches:
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                                       POTENTIAL.
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                                                                     53986 MW;
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793.00
53.71%
36.40%
33.93%
                                                      481
                                                                         481 AA;
                                                                                                                                                                                 Best Local Similarity:
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1045 CTCGGGGACCGGCAGGATGCCTGCGAGGGCGACAGTGGGGGGGCCCATGGTCGCCTCCTTC 1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1165 AACTACGGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATCCATGGGCACATCAGA 1224
                                                                                                                                                                                                                                                            405 GluhlaLysLeuGluAspAlaCysGlnGlyAspSerGlyGlyFroHisValThrArgFhe 424
                                                                                                                                                                                                                                                                                                                                                                                   445 LysTyrGlylleTyrThrLysValThrThrPheLeuLysTrpIleAspArgSerMetLys 464
                                                                 351 ---MetThrGlnLysThrGlyIleValSerGlyPheGly-----ArgThrHisGluLys 367
                                                                                                                                                                                              ::: ||| ||| ||| GlyArgGlnSerAsn------IleLeuLysMetLeuGluValProTyrValAspArg 384
868 CAGGCCGGCCAGGAGACC---CTCGTGACGGGCTGGGGGCTACCACAGCAGCCGAGAGAAG 924
                                                                                                                                                                              925 GAGGCCAAGAGAAACCGCACCTTCGTCCTCAACTTCAAGATTCCCGTGGTCCCGCAC 984
                                                808 TCGCAGACCATAGTGCCCATCTGCCTCCCGGACAGCGGCCTTGCAGAGCGCGAGCTCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Coagulation factor X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 AA.
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InterPro; IPR000742; EGF-2.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR0012383; GLA_blood.
InterPro; IPR001254; Ser_protease_Iry.
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.216; ...
MGD; MG1.103107; F10.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam: PF00594; gla: 1.
Pfam: PF0089; trypsin: 1.
PRINTS: PR00122; CHYMOTRYPSIN.
PRINTS: PR0010; EGFBLOOD.
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; BC003877; AAH03877.1; -. HSSP; P00742; 1XKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1225 GACAAGGAAGCCCCC 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 AlaArgValGlyPro 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q99L32;
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241 CGCAGCGGCTGGGAGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AICIGIGACTICGAGGAGGCCAAGGAAATITICCAAAATGIGGATGACACACTGGCCTIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .21 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .81 AGCCTGTGCGGGCACGGCACGTGCATCGACGCCATCGGCAGCTTCAGCTGCGACTGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 AlaSerGlyTyrPheLeuGlyAsnAspGlyLysSerCysIleSerThrAlaProPhePro 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------CGG 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 IleGluLeuLeuAsnLeuAsnGluThrGlnProGluArgSerSerAspAspLeuValArg 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508 CTCATTGATGGGAAGATGACCAGGCGGGGAGACAGCCCCTGGCAGGTGGTCCTGCTGGAC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     568 TCAAAGAAGAAGCTGGCCTGCGGGGCAGTGCTCATCCACCCCTCCTGGGTGCTGACAGCG 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SMOULD1; EGF. 1.

SMART; SMOUD01; EGF. 1.

SMART; SMOUD09; EGF. 1.

SMART; SMOUD09; EGF. 1.

PROSITE; PSOUD10; ATYP. SPC; 1.

PROSITE; PSOUD10; ATYP. CEF. 1.

PROSITE; PSOUD10; ATYP. CEF. 2.

PROSITE; PSOUD18; EGF. 2.

PROSITE; PSOUD18; EGF. 2.

PROSITE; PSOUD19; EGF. 2.

PROSITE; PSOUD14; EGF. 2.

PROSITE; PSOUD14; TRYPSIN. DOM; 1.

PROSITE; PSOUD14; TRYPSIN. DOM; 1.

PROSITE; PSOUD135; TRYPSIN. LIS; UNKNOWN. 1.

PROSITE; PSOUD135; TRYPSIN. SER; 1.

Calcium.-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCCTGGAGCGGGGAGTGCATAGAGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACAACGGGGGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGCTGTAGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;
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Conservative:
Mismatches:
Indels:
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793.00
53.718
36.408
SMART; SM00181; EGF; 2.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine protease
SEQUENCE 481
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985 AATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCTGAGAACATGCTGTGTGCGGGCATC 1044
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                   425 LysAsnThrTyrTyrValThrGlyIleValSerTrpGlyGluGlyCysAlaArgLysGly 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 LysTyrGly1leTyrThrLysValThrThrPheLeuLysTrpIleAspArgSerMetLys 464
                                                                                                          LysGluGluGlyAsnGluMetValHisGluValAspValValIleLysHisAsnLysPhe 311
                                                                                                                                               748 AGCAAGAGCACCACCGACAATGACATCGCACTGCTGCACCTGGCCCAGCCCGCCACCTC 807
                                                                                                                                                                  808 TCGCAGACCATAGTGCCCATCTGCCTCCCGGACAGCGGCCTTGCAGAGCGCGGAGCTCAAT 867
GCCCACTGCATGGATGAGTCCAAGAAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGG 687
                                                                                                                                                                                                                                                                                                                                                                          GAGGCCAAGAGAAACCGCACCTTCGTCCTCAACTTCATCAAGATTCCCGGTGGTCCCGCAC 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                            ---MetThrGlnLysThrGlylleValSerGlyPheGly-----ArgThrHisGluLys
                                                                                                                                                                                                                                                                                                CAGGCCGCCCAGGAGACC --- CTCGTGACGGGCTGGGGCTACCACAGCAGCCGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                           368 GlyArgGlnSerAsn-----IleLeuLysMetLeuGluValProTyrValAspArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405 GlualaLysLeuGluAspAlaCysGlnGlyAspSerGlyGlyProHisValThrArgPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1105 CACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGGGGGTGAGGGCTGTGGGCTCCTTCAC
                                                                       688 CGCTGGGAGAGTGGGAGCTGGACCTGGACATCAAGGAGGTCTTCGTCCACCCCAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sheehan J., Templer M., Gregory M., Hanumanthaiah R., Troyer D., Phan T., Thankavel B., Jagadeeswaran P.;
"Demonstration of the extrinsic coagulation pathway in teleostei: Identification of zebrafish coagulation factor VII.";
Proc. Natl. Acad. Sci. U.S.A. 98:8768-8773(2001).

EMBL; AX040345; AAK74192.1;

MEROPS; S01.215;
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InterPro; IPR001881; EGF_Ga.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interPro; IPR000561; EGF-like.
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 CGCTGTAGCTGTGCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 AsnCysSerCysAlaAspGlyTyrTyrLeuAspAsnSerGlyGlnLysCysArgSerHis 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 GTGAAGTTCCCTTGTGGGAGG---CCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 GluValPheProCysGlyLysValProLeuLeuGlnAlaGlyLysAlaAlaAspHis--- 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 TICTGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    520 AAGATGACCAGGCGGGAGACAGCCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            640 GATGAGTCCAAGAAGCTCCTTGTCAGGCTT-----GGAGAGTATGACCTGCGGCGCGTGG 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGAAGTGGGAGCTGGACCTGGACATCAAGGAGGTCTTCGTCCACCCCCAACTACAGGAG 753
                                                                                                                                                                                                                                                                                                                                                                            95
                                                                                                                                                                                                                                                                                                                                                           1 GCCAACTCC---TTCCTGGAGGAGCTCCGTCACAGCAGCGGGAGGGGGGAGTGCATAGAG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 GACTGCCGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 580 CTGGCCTGCGGGCAGTGCTCATCCACCCTGGGTGCTGACAGCGGCCCACTGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 PheTrpLyslleTyrAspValLysAspHisCysAlaSerSerProCysGluHis----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 GCCAGCCTGTGCTGCGGCACGCCACGTGC---ATCGACGGCATCGGCAGCTTCAGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATTGCTCGCTGGACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGG
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                                                                                                                                                                        CD9D1B179601BA4C CRC64;
                                                                                                                                                                                                                     433
165
69
144
12
pfam; PF00008; EGF; 2.
Pfam; PF00594; qla; 1.
Pfam; PF00089; trypsin; 1.
SMART; SM00179; EGF_CA; 2.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS0108; EGF_2; UNKNOWN_2.
PROSITE; PS01018; EGF_2; UNKNOWN_1.
PROSITE; PS01011; GLU_CARBOXILATION; UNKNOWN_1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00135; TRYPSIN_LHIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                    Conservative:
Mismatches:
                                                                                                                                                                                                                     Length:
Matches:
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                                                                                                                                                                        48680 MW;
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787.00
56.80%
40.05%
33.68%
                                                                                                                                                                        433 AA;
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                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                              Query Match:
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RA HU Z., Garen A.;

RT "Targeting tissue factor on tumor vascular endothelial cells and tumor calls for immunotherapy in mouse models of prostatic cancer.";

Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).

EMBL; AF72774; AR558668.1; -.

EMBL; AF77774; AR558668.1; -.

InterPro; IPR001512; ASX.hydroxyl.

InterPro; IPR00154; EGF_2.

DR InterPro; IPR001881; EGF_2.

DR InterPro; IPR001881; EGF_2.

DR InterPro; IPR001881; EGF_2.

DR InterPro; IPR001881; EGF_2.

DR InterPro; IPR001891; EGF_2.

DR Pfam; PF00089; EGF; 2.

DR Pfam; PF00089; EGF; 2.

DR Pfam; PF00089; trypsin; 1.

DR Pfam; PF00089; trypsin; 1.

DR SMART; SW00101; ASX_HYDROXXL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                 994 AGCGAGGTCATGAGCAACATGGTGTTCTGAGAACATGCTGTGTGCGGGCATCCTCGGGGAC 1053
                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCAGGATGCCTGCGAGGGCGACAGTGGGGGGCCCCATGGTCGCCTCCTTCCACGGCACC 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1114 TGGTTCCTGGTGGCCCTGGTGAGCTGGGGTGAGGCTGTGGGCTCCTTCACAACTACGGC 1173
                                                                                                                                                                                                                                                                                                                                                                     353 ValGlnValSerAsnLeuThrLeuThrSerAsnMetPheCysAlaGlyTyrIleGluGly 372
                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrSerArg-----LeuLeuArgArgLeuLeuValProArgIleArgThrGlnGluCys 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaPheLeuLeuGlyIleValSerTrpGlyLysGlyCysAlaArgProGlySerTyrGly 412
259 GluGlyThrGluGlnLeuIleGlnValAspGlnMetPheThrHisProAlaTyrValSer 278
                                                                                                                                                                                                                                319 SerLysHisThr---ValSerGlyTrpGly-----LysArgSerGluAspGlyPro 334
                                                                                                                                                                                                                                                                      934 AGAAACCGCACCTTCGTCCTCAACTTCATCAAGATTCCCGTGGTCCCGCACAATGAGTGC 993
                                                                                                                                     754 AGCACCACCGACAATGACATCGCACTGCTGCACCTGGCCCAGCCCGCCACCCTCTCGCAG
                                                                                                                 814 ACCATAGTGCCCATCTGCCTCCGGACAGCGGCCTTGCAGAGCGCGGAGCTCAATCAGGCC
                                                                                                                                                                                            874 GCCCAGGAGACCCTCGTGACGGGCTGGGGCTACCACAGCAGCCGAGAGGAGGAGGCCAAG
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Factor VII active site mutant immunoconjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00022; EGF_1; UNKNOWN_1.
PS01186; EGF_2; UNKNOWN_1.
PS01187; EGF_CA; UNKNOWN_1.
PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
PS000290; IG_MIC; UNKNOWN_1.
PS50240; TRYPSIN_DOM; 1.
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MEDLINE-21477448; PubMed-11593034;
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                                                                                                                                                                                                                                                                                                                                                                                         .81 AGCCTGTGCTGCGGGCACGGCACGTGCATCGACGGCATCGGCAGCTTCAGCTGCGACTGC 240
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                                                                                                                                                                                                                   61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC
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                                           94AC6CEB42CC992F CRC64;
                                                                                      701
164
75
148
36
                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                      Length:
Matches:
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1
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                          Hydrolase; Serine protease.
SEQUENCE 701 AA; 77826 MW;
                                                                                     1.23e-48
781.00
56.50%
38.77%
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1171 GGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATCCATGGGCACATCAGAGACAAG 1230
                                                                                                    946 ITCGTCCTCAACTTCATCAAGATTCCCGTGGTCCCGCAAATGAGTGCAGCGAGGTCATG 1005
                                                                                                                                                                                                                                        1051 GACCGGCAGGATGCCTGCGAGGGCGACAGTGGGGGGCCCCATGGTCGCTCCTTCCACGGC 1110
                                                                                                                                                                         ---AGCAACATGGTGTCTGAGAACATGCTGTGTGCGGGCATCCTCGGG 1050
                                                                                                                            LeuGluLeuMetValLeuAsnValProArgLeuMetThrGlnAspCysLeuGlnGlnGer 374
321 LeuCysLeuProGluArgThrPheSerGluArgThrLeuAlaPheVal---ArgPheSer 339
                                886 CTCGTGACGGGTTGGGGCTACCACAGCAGCGAGAAAGGAGGCCCAAGAGAAACCGCACC 945
                                                                                                                                                                                                                                                                                                                                                                                                375 ArgLysValGlyAspSerProAsnIleThrGluTyrMetPheCysAlaGlyTyrSerAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ornithorhynchus anatinus (Duckbill platypus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21015017; PubMed-11132153;
Poorafshar M., Aveskogh M., Munday B., Hellman L.;
Identification and structural analysis of four serine proteases impondereme, the platypus, Ornithorhynchus anatinus.";
Immunogenetics 52:19-28(2000).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                340 LeuValSerGlyTrpGlyGlnLeuLeuAspArgGlyAlaThrAla----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
coagulation factor X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 AA.
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SMART; SM00109; EGF_Like; 2.
SMART; SM00069; EGF_Lixe; 2.
SMART; SM000069; TYPE_SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
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InterPro; 1PR001314; Chymotrypsin.
InterPro; 1PR001314; Chymotrypsin.
InterPro; 1PR00184; EGF_2.
InterPro; 1PR001881; EGF_Ca.
InterPro; 1PR001881; EGF_Ca.
InterPro; 1PR001254; Ser_protease_Try.
InterPro; 1PR001254; VitK_dep_GLA.
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Pfam; PF00594; gla; 1.
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181 AGCCTGTGCGGGCACGGCACGTGCATCGACGGCATCGGCAGCTTCAGCTGCGACTGC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 SerAlaGlyTyrGluGlyLysAsnCysAspThrThrThrValLysIle---CysSerLeu 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 AlaGlnGlyTyrIleLeuGlyAspAspGlnLysSerCysIleProThrValProPhePro 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 CysGlyLysLeuThrValGlyArgArgLysArgSerArgGluLeuProGluGluGlnAsp 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454 -----CGCAGTCACCTGAAACGAGAC------ACAGAAGACCAAGAAGACCAA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 GluProProAspGlnAsnThrThrLeuAlaGluProGlyGluAsnAlaLeuValArqIle 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   511 ATTGATGGGAAGATGACCAGGCGGGGAGACAGCCCCTGGCAGGTGGTCCTGCTG---GAC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             568 TCAAAGAAGAAGCTGGCGGGGGGAGTGCTCATCCACCCTCCTGGGTGCTGACAGCG 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 GluAsnGlyGlnGlyPheCysGlyGlyThrIleLeuAsnGluTyrTyrIleLeuSerAla 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 AlaHisCysMetHisGlnAlaLysArgPheLysValArgValGlyGluArgAspThrGlu 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCTGGGAGAAGTGGGAGCTGGACCTCGACATCAAGGAGGTCTTCGTCCACCCCAACTAC 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :::||||:::
192 GlyAspAsnAlaHisValAlaGluAspValLeuGluAlaThrGluAsnProPheGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGCTGTAGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                       1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCCTGGAGCGGGAGTGCATAGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||::: ::: ||||||::||||||
81 TrpAsnIleTyrLysAspGlyAsnGlnCysGluThrGlnPro-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCACTGCATGGATGAGTCCAAGAAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGG
                                                                                                                                                          4C66C230D0758F6A CRC64;
                                                                                                                                                                                                                469
162
74
157
50
                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 TGTGGGAGCCCTGGAAGCGGATGGAGAAGAAG------
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS0011; GLU_CARBOXYLATION; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_LISU UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_LIS; 1.
Hydrolase; Serine protease;
                                                                                                                                                                                                                Length:
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                                                                                                                                                          52196 MW;
                                                                                                                                                                                                              4.39e-48
773.00
53.27%
36.57%
33.08%
                                                                                                                                                      469 AA;
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                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                           Query Match:
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982 CACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCTGAGAACATGCTGTGTGCGGGC 1041
                                                                                                                                                                                                                                                                                                                                                                         1102 TTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGGGGTGAGGGCTGTGGGCTTCTT 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1162 CACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATCCATGGGCACATC 1221
                                                                                                                                                                                                                                                                                                                                                                                          384 ArgThrThrCysLysGlnSerSerSerPheAspIleThrProAsnMetPheCysAlaGly 403
::: ::: ||||| |||||| ::: 292 LysLysAspSerSerGluMetAlaHisGluValGluLysValIleValHisSerLysPhe 311
                                               748 AGCAAGAGCACCGCGACAATGACATGGCACTGCTGCACCTGGCCCAGCCCGCCACCCTC 807
                                                                               312 ValLysLysThrTyrAspPheAspIleAlaValIleLysLeuLysThrProIleThrPhe 331
                                                                                                               808 TCGCAGACCATAGTGCCCATCTGCCTCCGGACAGCGGCCTTGCAGAGCGCGGAGCTC--- 864
                                                                                                                                  865 ---AATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGGGGCTACCACAGCAGCGGAGG 921
                                                                                                                                                                                                922 AAGGAGGCCAAGAGAACCGCACCTTCGTCCTCAACTTCATCAAGATTCCCGTGGTCCCG 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of a cDNA encoding murine coagulation factor VII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thromb. Haemost. 75:481-487(1996).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D., Castellino F.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     446 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequ 01-JUN-2002 (TrEMBLrel. 21, Last anno Coaquilation factor VII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR000152; Asx_hydroxyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asx_hydroxyl.
Chymotrypsin.
Crystallin.
EGF-like.
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MEDLINE=96276538; Pubmed=8701412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001064; C
InterPro; IPR000561; E
InterPro; IPR001881; E
InterPro; IPR002383; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; S01.215; -. MGD; MGI:109325; F7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1222 AGAGACAAG 1230
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Q61109
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GLA blood

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R SMART; SMO0179; EGF_CA; 1.

R SMART; SMO0179; EGF_CA; 1.

R SMART; SMO0001; EGF_LIKe; 1.

R SMART; SMO00020; EGF_LIKe; 1.

R PROSITE; PSO00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.

R PROSITE; PSO0025; CRYSTALLIN_BETAGAMAA; UNKNOWN_1.

R PROSITE; PSO1025; EGF_L; UNKNOWN_1.

R PROSITE; PSO1025; EGF_CA; 1.

R PROSITE; PSO1187; EGF_CA; 1.

R PROSITE; PSO101187; EGF_CA; 1.

R PROSITE; PSO101187; EGF_CA; 1.

R PROSITE; PSO101187; EGF_CA; 1.

R PROSITE; PSO10137; EGF_CA; 1.

R PROSITE; PSO10134; TRYPSIN_DOM; 1.

R PROSITE; PSO10135; TRYPSIN_HIS; 1.

R PROSITE; PSO10135; TRYPSIN_HIS; 1.

R Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 AGCCTGTGCTGCGGCCACGCACGTGCATCGACGGCATCGGCAGCTTCAGCTGCGACTGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 AsnVal------GlyThrCysGlnAspHisLeuLysSerTyrValCysPheCys 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 CTGGACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGCC---TGT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------ArgileValGlyGlyAsnValCysProLys 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535 GGAGACAGCCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGCTGGCCTGCGGGGCA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 GlyGluCysProTrpGlnAlaVal---LeuLysIleAsnGlyLeuLeuLeuCysGlyAla 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 TrpileValTyrSerAspGlyAspGlnCys-----AlaSerAsnProCysGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 AGCTGTGCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                475 ACAGAAGACCAAGAACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGG
                                                                                                                                                                                                                                                                                                                                                                             446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;
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163
74
147
36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00594; 9la; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-763-153-1 (1-1245) x Q61109 (1-446)
                                                                                     PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                             5.15e-48
772.00
56.43%
38.81%
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                                                                                                                                                                                                                                                                                                                                                              Serine protease
SEQUENCE 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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946 TICGTCCTCAACTICATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGGGGGGTCATG 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ATGGĮGTCTGAGAACATGCTGTGTGCGGGCATCCTCGGG 1050
                  |||||||::
| 222 ValLeuLeuAspAlaArgTrpIleValThrAlaAlaHisCysPheAspAsnIleArgTyr 241
                                                                                                                                    706 CIGGACCTGGACATCAAGGAGGTCTTCGTCCACCCCAACTACAGCAAGAGCACCACCGAC 765
                                                                                                                                                                                                                                                                                               :::||||||||||::: :::|||| 302 LeuCysLeuProGluLysSerPheSerGluAsnThrLeuAlaArgIle----ArgPheSer 320
                                                                                                                                                                                                                                                                                                                                               886 CTCGTGACGGGCTGGGGCTACCACAGCGGGGGGAGAAGGAGGCCAAGAGAAACCGCACC 945
                                                                                                                                                                                                                                                                                                                                                                                  321 ArgvalSerGlyTrpGlyGlnLeuLeuAspArgGlyAlaThrAla----- 335
                                                                                                                                                                                                                                                                                                                                                                                                                                           356 LysHisSerSerAsnThrProLysIleThrGluAsnMetPheCysAlaGlyTyrMetAsp 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 GlyThrLysAspAlaCysLysGlyAspSerGlyGlyProHisAlaThrHisTyrHisGly 395
                                                                                        242 TrpGlyAsnileThrValValNalNdGlyGluHisAspPheSerGluLysAspGlyAspGlu 261
                                                                                                                                                                     262 GlnValArgArgValThrGlnValIleMetProAspLysTyrIleArgGlyLysIleAsn 281
                                                                                                                                                                                                         AATGACATCGCACTGCTGCACCTGGCCCAGCCCGCCACCTCTCGCAGACCATAGTGCCC 825
                                                                                                                                                                                                                            GTGCTCATCCACCCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAG--- 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        652 -----AAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGGCGCTGGGAGAAGTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Satta \mathbf{r}_{\cdot,\cdot} "Comparison of DNA and protein polymorphims between humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes Genet. Syst. 0:0-0(2001).
EMBL; AB062470; BAB58885.1; --
EMBL; AB062458; BAB58885.1; JOINED.
EMBL; AB062466; BAB58885.1; JOINED.
EMBL; AB062466; BAB58885.1; JOINED.
EMBL; AB062464; BAB5885.1; JOINED.
EMBL; AB062466; BAB5885.1; JOINED.
EMBL; AB062466; BAB5885.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000152; Asx_hydroxyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coagulation factor XI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1006 AGCAAC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9598;
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 595
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73 GAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTCTGGTCCAAGCAC 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 CysGluGlnPheCysLysAsnSerAlaAspAsnLysValValCysSerCysThrGluGly 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 TACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCTTGTGGGAGG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CysLeu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 AsnGlyGlySerCysLysAspAspIleAsnSerTyrGluCysTrpCysProPheGlyPhe 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 GAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTGGACAACGGCGGC 312
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201 TyrValAsnSerThrGluAlaGluThrIleLeuAspAsnIleThrGlnSerThrGlnSer 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ValSerValSerGlnThrSerLysLeuThrArgAlaGluThrValPheProAspValAsp 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 PheAsnAspPheThrArgValValGlyGlyGluAspAlaLysProGlyGlnPheProTrp 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         550 CAGGIGGICCIGCIGGACICAAAGAAGAAGIGGCCIGCGGGGGGAGIGCICAICCACCCC 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 CTGGAGGAGCTCCGTCACCAGCAGCCTGGAGCGGGAGTGCATAGAGGAGATCTGTGACTTC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 GluGluAlaArgGluValPheGluAsnThrGluArgThrThrGluPheTrpLysGlnTyr 91
                                                                                                                                                                                                                                                                                    51764 MW; 30C2F857C0F77F45 CRC64;
                                                                                                                                                                                                                                                                                                                                         461
151
71
71
156
46
                                                                         Pfam: PF00008; EGF; 2.
Pfam: PF00008; EGF; 2.
Pfam: PF00089; Lrypsin: 1.
PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE: PS01080; EGF_1; UNKNOWN_2.
PROSITE: PS01180; EGF_2; UNKNOWN_2.
PROSITE: PS01180; EGF_2; UNKNOWN_1.
PROSITE: PS01181; EGF_CA; UNKNOWN_1.
PROSITE: PS000113; EGF_CA; UNKNOWN_1.
PROSITE: PS000134; TRYPSIN_DOM; 1.
PROSITE: PS00134; TRYPSIN_LOM; 1.
PROSITE: PS00134; TRYPSIN_LOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 ValAspGlyAspGlnCysGluSerAsnPro-------
                                                                                                                                                                                                                                                                                                                                                                          Conservative;
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                       Matches:
                                                                                                                                                                                                                                                                                                                                         Length:
            InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; Vitk_dep_GLA.
Pfam. PR000009.
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InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                  Hydrolase; Serine protease. SEQUENCE 461 AA; 51764 M
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52.36%
35.61%
31.66%
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958 TICATCAAGATICCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTG 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1078 AGTGGGGGGCCCATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGGCCTGGTGAGC 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLEEL. 01, Created)
01-NOC-1999 (TrEMBLEEL. 11, Last sequence update)
01-JUN-2002 (TrEMBLEEL. 21, Last annotation update)
199 (Coagulation factor IX (Plasma THROMBOPLASTIC component, christmas disease, HAEMOPHILIA B)) (Factor IX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 TyrAsnAsnMetPheCysAlaGlyPheHisGluGlyGlyAIyArgAspSerCysGlnGlyAsp 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---AlaLeuValLeuGln 370
                   784 CACCTGGCCCAGCCCGCCACCCTCTCGCAGACCATAGTGCCCATCTGCCTCCCGGACAGC 843
                                                                                                                                                                                                                      844 GGCCTTGCAGAGCGCGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGGGGC 903
                                                                                                                                                                                                                                                                                                 340 GluTyrThrAsnIlePheLeuLysPheGly-----SerGlyTyrValSerGlyTrpGly 357
                                                                                                                                                                                                                                                                                                                                   904 -----TACCACAGCAGAGAGAAGGAGGCCAAGAAACCGCACCTTCGTCCTCAAC 957
610 TCCTGGGTGCTGACAGCGGCCCACTGCATGAGTCCAAGAAGCTCCTTGTCAGGCTT 669
                                                                                                                                  730 TTCGTCCACCCCAACTACAGCAAGAGCACCAC-----GACAATGACATCGCACTGCTG 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The putative factor IX gene promoter in hemophilia B Leyden.";
Blood 72:1074-1076(1988).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                 670 GGAGAGTATGACCTGCGGCGCTGGGAGAGTGGGAGCTGGACCTGGACATCAAGGAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reitsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bird C.; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         456 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                    358 ArgValPheHisLysGlyArgSer--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRYPSIN FAMILY.
EMBL; AL033403; CAA21954.1; -.
EMBL; X55008; CAB38245.2; -.
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176 ValSerValSerGlnThrSerLysLeuThrArgAlaGluThrValPheProAspValAsp 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 GICGACGGIGACCAGIGCIIGGICIIGCCCIIGGAGCACCCGIGCGCCAGCCIGIGCIGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 AsnGlyGlySerCysLysAspAspIleAsnSerTyrGluCysTrpCysProPheGlyPhe 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 GAGGGCCGCTTCTGCCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTGGACAACGGCGGC 312
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119 GluGlyLysAsnCysGluLeuAspValThr-----CysAsnIleLysAsnGlyArg 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 TGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGG---CGCTGTAGCTGTGCGCCTGGC 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 CCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGA---------471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcium-binding; EGF-like domain; Glycoprotein; Hydrolase; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----CysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 GGGCACGGCACGTGCATCGACGGCATCGGCAGCTTCAGCTGCGGACTGCGCAGCGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SMO020; TYP_SPC; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS00011; GLG_CABOXYLATION; 1.
PROSITE; PS00011; GLG_CABOXYLATION; 1.
PROSITE; PS00013; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                 MEMORY: SOLICIAL, INTERPRETOR IDENOUSES, BAX_hydroxyl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001861; EGF_1ike.
InterPro; IPR001881; EGF_G.
InterPro; IPR001881; EGF_II.
InterPro; IPR001383; GLA_blood.
InterPro; IPR001254; Ser_II.
InterPro; IPR0001254; Ser_II.
InterPro; IPR0001254; Ser_II.
InterPro; IPR0001254; Ser_II.
InterPro; IPR00010; EGF: 2.
INTERS; PR00010; EGFBLOOD.
INTERPRETOR INTERPROPERTOR INTERPRETOR INTERPROPERTOR INTERPRETOR INTERPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.16e-45
736.00
52.36%
35.38%
31.49%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp_SPc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity:
                     MEROPS; S01.214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1018 TCTGAGAACATGCTGTGTGCGGCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGGGGAC 1077
                           196 TyrvalAsnSerThrGluAlaGluThrIleLeuAspAsnIleThrGlnSerThrGlnSer 215
                                                                                                                                                                                                                                             GGAGAGTATGACCTGCGCGCTGGGAGAAGTGGGAGCTGGACCTGGACATCAAGGAGGTC 729
                                                                                                                                                                                                                                                                730 ITCGICCACCCCAACIACAGCAAGAGCACCACC-----GACAAIGACAICGCACIGCIG 783
                                                                                                                                                                                                                                                                                                                            366 TyrLeuArgValProLeuValAspArgAlaThrCysLeuArgSerThrLysPheThrIle 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 TyrasnasnactheCysalaGlyPheHisGluGlyGlyArgaspSerCysGlnGlyAsp 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 TrpGlyGluGluCysAlaMetLysGlyLysTyrGlyIleTyrThrLysValSerArgTyr 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          904 -----TACCACAGCAGCGAGAGAAGGAGGCCAAGAGAAACCGCACCTTCGTCCTCAAC 957
                                                                                  116 PheAsnAspPheThrArgValValGlyGlyGluAspAlaLysProGlyGlnPheProTrp
                                                                                                                     550 CAGGTGGTCCTGCTGGACTCAAAGAAGAAGCTGGCCTGCGGGGCAGTGCTCATCCACCCC
                                                                                                                                                236 GlnValVal---LeuAsnGlyLysValAspAlaPheCysGlyGlySerIleValAsnGlu
                                                                                                                                                                                510 ICCIGGGIGCIGACAGCGGCCCACIGCAIGGAIGAGICCAAGAAGCICCIIGICAGGCII
                                                                                                                                                                                                  784 CACCTGGCCCAGCCGCCACCTCTCGCAGACCATAGTGCCCATCTGCCTCCCGGACAGC
                                                          1138 IGGGGTGAGGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                               844 GGCCTTGCAGAGCGCGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
   -----GACACAGAAGACCAAGAAGACCAAGTAGAT--
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73 GAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTCTGGTCCAAGCAC 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 GGGCACGCCACGTGCATCGACGCCATCGGCAGCTTCAGCTGCGACTGCCGCAGCGGCTGG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 AsnGlyGlySerCysLysAspAspIleAsnSerTyrGluCysTrpCysProPheGlyPhe 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 GAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTGGACAACGGCGGC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 CysGluGlnPheCysLysAsnSerAlaAspAsnLysValValCysSerCysThrGluGly 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValSerValSerGlnThrSerLysLeuThrArgAlaGluThrValPheProAspValAsp 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 TACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCTTGTGGGAGG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIGGAGGAGCTCCGTCACAGCAGCCTGGAGCGGGAGTGCATAAGAGGAGATCTGTGACTTC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 TGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGG----CGCTGTAGCTGTGCGCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comparison of DNA and protein polymorphims between humans and chimpanzees.";

cense Genet. Syst. 0:0-0(2001).

EMBL: AB062471; BAB58886.1; -1

EMBL: AB062459; BAB58886.1; JOINED.

EMBL: AB062461; BAB58886.1; JOINED.

EMBL: AB062465; BAB58886.1; JOINED.

EMBL: AB062465; BAB58886.1; JOINED.

EMBL: AB062465; BAB58886.1; JOINED.

EMBL: AB062465; BAB5886.1; JOINED.

EMBL: AB062465; LAB58886.1; JOINED.

EMBL: AB062467; BAB5886.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                            8F5A69A525DF65B5 CRC64;
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149
67
162
46
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                    PFGOMMS; trypsin; 1.
PROSITE; PSOGOTI, ASX-HYDROXYL; UNKNOWN_1.
PROSITE; PSOGOTS; EGF 1; UNKNOWN_1.
PROSITE; PSO1186; EGF_2; UNKNOWN_2.
PROSITE; PSOGOTIS; EUL_CABROXYLATION; UNKNOWN_1.
PROSITE; PSOGOTI; GLU_CABROXYLATION; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                             UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                              UNKNOWN
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                                                                                                                                                                                                         Interpro; IPR001881; EGF_Ca.
Interpro; IPR001254; Ser_protease_Try.
Interpro; IPR000294; Vitk_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00594; gla; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-763-153-1 (1-1245) x Q95ND6 (1-461)
                                                                                                                                                              InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                            51695 MW;
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718.00
50.948
35.148
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                                                                                                                                                                                            InterPro; IPR000742; EGF_2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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1078 AGTGGGGGGCCCATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGGTGAC 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1018 TCTGAGAACATGCTGTGTGCGGGCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGCGAC 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 TGGGGTGAGGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCCAAAGTCAGCCGCTAC 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 ArgValPheHisLysClyArgSer---------AlaLeuValLeuGln 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| :::||| || ||| 330 GluLeuAspGluProLeuValLeuAsnSerTyrValThrProIleCysIleAlaAspLys 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          844 GGCCTTGCAGAGCGCGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGGGGC 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 TyrasnasnMetPheCysAlaGlyPheHisGluGlyGlyArgAspSerCysGlnGlyAsp 410
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240 Arg***ValValLeuAsnGlyLysValAspAlaPheCysGlyGlySerIleValAsnGlu 259
                                                                                                                                                                                                                                                            784 CACCTGGCCCAGCCGCCACCCTCTCGCAGACCATAGTGCCCATCTGCCTCCCGGACAGC 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 GluTyrThrAsnIlePheLeuLysPheGly-----SerGlyTyrValSerGlyTrpGly 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     904 -----TACCACAGAGAGGAGAGAAGGAGGCCAAGAGAAACGGAACTTCGTCCTCAAC 957
                                                                                                                                                          550 CAGGTGGTCCTGCTGGACTCAAAGAAGAAGCTGGCCTGCGGGGCAGTGCTCATCCACCCC 609
                                                                                                                                                                                                                                     610 TCCTGGGTGCTGACAGCGGCCCACTGCATGAGTCCAAGAAGCTCCTTGTCAGGCTT 669
                                                                                                                                                                                                                                                                                                                    670 GGAGAGTATGACCTGCGGCGCTGGGAGAGTGGGGAGCTGGACCTGGACATCAAGGAGGTC 729
                                                                                                                                                                                                                                                                                                                                                      280 GlyGluHisAsnIleGluGluThrGluHisThrGluGlnLysArgAsnValIleArglle 299
                                                                                                                                                                                                                                                                                                                                                                                             730 TTCGTCCACCCCAACTACAGCAAGAGCACCACC-----GACAATGACATCGCACTGCTG 783
---GACCAAGAA 489
                                       201 TyrValAsnSerThrGluAlaGluThrIleLeuAspAsnIleThrGlnThrProGlnSer 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Struthio camelus (Ostrich).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;
                                                                              490 GACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGGGGAGACAGCCCCTGG
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
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            Ogawa T.;
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       Frost C., Naude R., Oelofsen W., Muramoto K., Naganuma T., Oga "Purification and characterization of ostrich prothrombin.";
Int. J. Bacchem. Cell Biol. 32:1151-1159(2000).
ISMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS 'TRYBSIN FAMILY
EMBL' ABORSB871: BAAB9046.1; -.
MESSP, P00734; 1UVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69392 MW; 11B974B9AEE54EA2 CRC64;
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Mismatches:
                                                                                                                                                                                                                                                                                                                SMART; SM00069; GLA; 1.
SMART; SM000130; KR; 2.
SMART; SM000130; KR; 2.
SMART; SM00010; TYP_SPC; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS50070; KRINGLE_1; 2.
PROSITE; PS5040; TRYPSILL_DOM; 1.
PROSITE; PS5040; TRYPSILL_DOM; 1.
PROSITE; PS00134; TRYPSILL_DOM; 1.
PROSITE; PS00135; TRYPSILL_SER; 1.
Hydrolase; Serine protease.
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InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001294; VitK_dep_GLA.
Pfam; PF00594; gla; 1.
Pfam; PF00051; Kringle; 2.
Pfam; PF00089; trypsin; 1.
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MEDLINE=20579470; PubMed=11137455;
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InterPro; IPR002383; GLA_blood.
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PRINTS; PR00001; GLABALOD.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 2.
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525.00
39.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           642
                                                                                                                                                                                                                                                              481 GACCAAGAAGACCAAGTAGATCCGCGCTCATTGATGGGAAGATGACCAGGCGGGGAGAC 540
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                                                                                                       228 CysLeuProTrpAsnSerGluLysAlaLysGluValLeuGlnGlyLysThrIleIleThr 247
                                                                                                                                                                                                                   268 CysValThrAspGluProProHisPheGluTyrCysAspLeuGlnTyrCysAspSerSer 287
                                                                                                                                                                                                                                                                                                                             306 GluTyrLysThrPhePheAspAsp-----LysThrPheGlySerGlyGluAlaAspCys 323
                                                                                                                                                                                                                                                                                                                                                                                     324 GlylleArgPro-----LeuPheGluLysLysLysLyslleLysAspLysSerGluLysGlu 341
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188 GluArgThrThrValGluPheThrProArgValLysProProAlaSerThrGluProCys 207
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481 LeuAlaGlyTyrLysGlyArgValThrGlyTrpGlyAsnLeuLysGLuThrTrpAlaThr
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501 AsnProSerAsnLeuProThrValLeuGlnGlnLeuAsnValProIleValAspGlnAsp
                                                   208 GluGlnGluLysGlyMetLeuTyrAlaGlyThrLeuSerValThrIleSerGlyAlaLys
                                                                             232 TGC-------GACTGCCGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGC
                                                                                                                                                              248 GluValLysLeuLeuGluAsnTyrCysArgAsnProAspAlaAspAspGluGlyValTrp
                                                                                                                                                                                                                                                 -----CTAGAGGAGGTGGGCTGGCGGCGCTGTAGCTGTGCGCCT
                                                                                                                                                                                                                                                                                                     367 GGCTACAAG----CTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCTTGT
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                                                                                                                                    274 GAGGTGAGCTTCCTCAAT--
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Banfield D.K., Irwin D.M., Walz D.A., MacGillivray R.T.;
"Evolution of prothrombin: isolation and characterization of the cDNAs encoding chicken and hagfish prothrombin.";
J. Mol. Evol. 38:177-187(1994).
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Banfield D.K., MacGillivray R.T.; "Partial characterization of vertebrate prothrombin cDNAs: amplification and sequence analysis of the B chain of thrombin from
1153 GGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATC 1209
                                 581 AspargaspGlyLysTyrGlyPheTyrThrHisValPheArgLeuLysLysTrplle 599
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Banfield D.K.;
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
EMBL; M81391; AAA21619.1; -.
HSSP; P00734; 1UVS.
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Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992)
                                                                                                                                                                           607 AA.
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InterPro; IPR002383; GLA_blood.
InterPro; IPR000001; Kringle.
InterPro; IPR001956; Prothrombin.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; Vitk_dep_GLA.
Pfam; PF000594; glas; 1.
Pfam; PF000594; kringle; 2.
Pfam; PF00089; trypsin; 1.
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PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
FYORSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease.
SEQUENCE 607 AA; 69110 MW; 002F3606E&
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SMART; SMO0200; TTYP_SPC; 1.
PROSITE; PS00011; GLU_CARBOXYLATION;
PROSITE; PS00021; KRINGLE_1; 2.
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MEDLINE=94223694; PubMed=7513365;
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PRINTS; PR00001; GLABLOOD.
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ProDom; PD000395; Kringle; 2.
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                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                            Thrombin.
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		C 69 : n 67	П	s 87	- 132		· — >-	- 17	e 147	- 17	p 167	- 19	n 187	G 25	r 20	G 300	,	s 24	G 33	p 26	<b>(</b> )	s 27	4 (	667		າ	A 46:	c 528 a 357
607 156 168 174 20		TTCTGGAGGAGCTCCGTCACAGCAGCCTGGAGCGGGAGTGCATAGAGGAGATCTGTGAC	TTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTCTGGTCCAAG	TyrGluGluAlaPheGluAlaLeuGluSerThrValAspThrAspAlaPheTrpAlaLys		TyrGlnValCysGlnGlyThrLysMetProArgThrThrLeuAspAlaCysLeuGluGly	AsnCysAlaAlaAsnLeuGlyGlnAsnTyrArgGlyThrIleAsnTyrThrLysSerGl		IleGluCysGlnValTrpThrSerLysTyrProHisIleProLysPheAsnAlaSerIl		TyrProAspLeuThrGluAsnTyrCysArgAsnProAspAsnAsnSerGluGlyProTr	-TGCGCCAGCCTGTGCGGG	CysTyrThrArgAspProThrValGluArgGluGluCysProIleProValCysGlyGln	CACGGCACGTGCATCGGCATCGGCAGCTTCAGCTGCGACTGCCGCAGCGGCTGGGAG	-PheThrProArgValLysProSerThrThr	GGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTG [1]::		 erGlyAlaArgCysLeuProTrpAlaSerGluLysAlaLysAlaLeuLeuGlnAspLy	GAG	:::        :::  ThrIleAsnProGluValLysLeuLeuGluAsnTyrCysArgAsnProAspAlaAspAs	-cctggctacaagctgggggac	CysValIleAspGluProProTyrPheGluTyrCy	GACCTCCTGCAGTGTCACCCCGCAGTG	IIIValeideidileat	[ ] [ ] [ ] O d G = d H o s	organ grant arectico and takine ng santa kine kine kine ng santang santa kine organ sa ng r	-AGGCCCTGGAAGCGGATGGAGAAGCGCAGTCACCTGAAA        	CGAGACACAGAAGACCAAGAAGACCAAGTAGATCCGCGGCTCATTGATGGGAGATGACC ::::
: ative: hes:		SAGTGC/        GluCys]	GACACA	AspThri		ThrLeu	rhr11e		IlePro		AspAsni	recece	JysPro	FGCGAC:	ProArg	TGAGC:		AlaLys/	FGCCTA	CysArg/	CCT(	31uProl		n tones	1	nspera	GAGAAGAAGC             GluLysLysG	CGCCTC2
Length: Matches: Conservativ Mismatches: Indels: Gaps:	_	GAGCGG	GTGGAT	Thrval		ArgThr	ArgGly'	900	ProHis		AsnPro	:	GluGlu	TTCAGC	PheThr	LeuTvr	1 1	GluLys	-ACGCATTACTGCCTA	AsnTyrCys	1	IleAsp	1 (	n rodeu	Chacha	FIIGFIIE	CGGATG	GATCCG
пхохно	(1-607)	CAGCCTG :::    /AsnLeu	CAAAAT	ıGluSer		SMetPro	AsnTyr	GAGCAC	LysTyr		CysArg		lGluArg	GGCAGC		sGlvMet	, ;	AlaSer	ACG	lLeuGlu	TGTGCG	·Cysval	AGTG		remp.	ın i e kırı	TGGAAG	CAAGTA ::: TyrMet
4.55e-29 512.00 39.25% 27.71% 21.91%	091001	STCACAGO LeLysGl	AAATTTT(	luAlaLe		lyThrLy	euGlyGlı	PGCCCTT	rpThrSe		uAsnTy		roThrVa	ACGGCAT(	;	GGAG      erglutys	' !	euProTri		ılLysLe	SCTGTAG	1	ACCCCGC.	ביים ביים ביים	, dan 194	TIOT OF THE	AGGCCC        hrArgPro	AGGAGA( ::: etAspSei
511. 272. 271. 131.	5) x	CTCC( ::: MetI	AAGG	PheG		GlnG	AsnLe	GTCT	ValTı		ThrG		AspPı	ATCGAC:	Valg]	CAGC(:::	TGC	Cysle		GluVa	රපුවර	-	TGTC2	- I	[ Seda	9	666	SACC! LeuMe
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	-1 (1-124	TGGAGGAG              euGluGlu	AGGAGGCC	luGluAla	1	lnvalcys	ysAlaAla	GACCAGIGCTIGGTCTIGCCCTIGGAGCACCCG	lucysGln		roAspLeu		yrThrArg	GCACGTGC	GluArgThrThrValGlu	GGCCGCTTCTGCCAGCGCGAG    ::    ::     GlvGlnProCvsGluSerGluLv	GACAACGGCGGCTGC	lyAlaArg		leAsnPro	GAGGTGGCCTGCCGCTGTAGCTGTGCG-	GluGlyValTrp-	GACCTCCTGCAGTGTCACCCCGCAGTG	TI CTUDO	rampr110	911111161	AAGTICCCTTGTGGGAGGCCC ::: GluAlaAspCysGlyThrArgPro	ACACAGAA ::      :luLysGlu
Scor mila Sim	-153-	TTCC	TTCG	Tyre	CAC-	TyrG	AsnC	GACC	IleG	;	TyrF	:	CysT	CACG	GluA	66CC(	GACA	SerG	;	Thri	GAGG	GluG	GACC		40.0	9175	AAGT ::: GluA	CGAG : SerG
ignment ed. No.: ore: rcent Si st Local ery Matc	-763	10	70	68	130	133	108	142	128	174	148	175	168	196	188	256	301	224	316	244	m s	264	385	41.	300		412	338
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1036 GCGGGCATCCTCGGGGAC------CGGCAGGATGCCTGCGAGGGCGACAGTGGGGGG 1086
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                                                              639
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                                                                               398 ProProTrpAspLysAsnLeuThrThrAsnAspIleLeuValArgMetGlyLeuHisPhe 417
                                                                                                                                                                                                                                                                                                                            796 CCCGCCACCCTCTCGCAGACCATAGTGCCCATCTGCCTCCCGGACAGCGCCTTGCAGAG 855
                                                                                                                                                                                                                                                                                                                                               856 CGCGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGGGGCTACCACAGCAGC 915
                                                                                                                                                                                                                                                                                                                                                                                                            916 CGAGAGAAGGAGGCCAAGAGAAACCGCACCTTCGTCCTCAACTTCAAGATTCCCGTG 975
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537 AlaGlyTyrSerProGluAspSerLysArgGlyAspAlaCysGluGlyAspSerGlyGly 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       529 AGGCGGGGAGACAGCCCCTGGCAGGTGGTCCTGCTG----GACTCAAAGAAGATGGCC 585
                  ------GATGAG------TCCAAGAAGCTCCTTGTCAGGCTTGGAGAGTATGAC 681
                                                                                                                                                                                               682 CTGCGGCGCTGGGAGAAG---TGGGAGCTGGACCTGGACATCAAGGAGGTCTTCGTCCAC 738
                                                                                                                                                                                                                            418 ArgAlaLySTyrGluArgAsnLySGluLySIleValLeuLeuAspLySValIleIleHis 437
                                                                                                                                                                                                                                                                                         438 ProLysTyrAsnTrpLysGluAsnMetAspArgAsplleAlaLeuLeuHisLeuLysArg 457
                                                                                                                                                                                                                                                            CCCAACTACAGC --- AAGAGCACCACCGACAATGACATCGCACTGCTGCACTGGCCCAG 795
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MEDLINE=21085660; PUDMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OgDBIO;

Ol-JUN-2001 (TrEMBLrel. 17, Created)

Ol-JUN-2001 (TrEMBLrel. 17, Last sequence update)

Ol-JUN-2002 (TrEMBLrel. 21, Last annotation update)

1300008A22Rik protein.

Mus musculus (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                              TGGGGGGCAGTGCTCATCCACCCTCCTGGGTGCTGACAGCGGCCCACTGCATG-----
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SEQUENCE FROM N.A.
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Radota T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Rabburner M., Batalov S., Casavant T.,
Rak Kuehl P., Lewis S., Matsuo Y., Mikaido I., Pesole G., Quackenbush J.,
Schrim L. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carnincl P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whynshaw-Bonis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Wanshay-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 GCCAGCCTGTGCTGCGGCACGCACGTGCATC-----GACGCCATCGCCAGCTTC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 AGCTGCGACTGCCGCAGCGGCTGGGAGGCCCGTTCTGCCAGCGCGAGGTGAGCTTCCTC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 CGCTGTAGCTGTGCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCGGCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 TTCTGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 AATTGCTCGCTGGACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGG
                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-: SIMILARITY: CONTAINS 1 CUB DOMAIN.
-: SIMILARITY: BELONGS TO PEFTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||||| :::||| |||:::
|GluPheLeuCysSerValAsnGlyLeuCysValProAlaCysAspGlyIleLys-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Hydrolase; Serine protease.
SEOUENCE 799 AA; 89557 MW; 16315A646A4D5288 CRC64;
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137
52
141
63
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Mismatches:
Indels:
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Matches:
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PROSITE; PS50060; LDLRA_2; 3.
PROSITE; PS50200; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001859; CUB_domain.
InterPro; IPR002172; LDL_recept_A.
InterPro; IPR001254; Ser_protease_Try.
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PRINTS; PR00261; IDLRECEPTOR.
SMART; SM00042; CUB. 1.
SMART; SM000192; IDLA: 3.
SMART; SM00020; Tryp_SPc; 1.
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510.50
48.09%
34.86%
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sest Local Similarity:
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1111 ACCTGGTTCCTGGTGGGCCTGGTGAGCTGGGGTGAGGGCTGTGGGCCTCCTTCACAACTAC 1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               994 AGCGAGGICAIGAGCAACAIGGIGICIGAGAACAIGCIGIGIGCGGGCAICCICGGGGAC 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        722 SerGluAlaTyrArgTyrGlnValSerProArgMetLeuCysAlaGlyTyrArgLysGly 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        705 SerAsn-----ThrLeuGlnLysValAspValGlnLeuValProGlnAspLeuCys 721
                                                                                                                                                                                                                                                                      754 AGCACCACCGACAATGACATCGCACTGCTGCTGGCCCAGCCCAGCCCGCCACCTTCGCAG 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             814 ACCATAGTGCCCATCTGCCTCCGGACAGCGGCCTTGCAGAGCGCGAGCTCAATCAGGCC 873
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409 GIGAAGTICCCIIGIGGGAGGCCCIGGAAGCGGAIGGAGAAGAAGCGCAGICACCIGAAA 468
                                                                                                                    534 LysProAsnProGluCysAspGlyGlnSerAspCysArgAspGlySerAspGluGlnHis 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      687 GlyGlnHisCysTrpIleThrGlyTrpGly-----AlaGlnArgGluGlyGlyProVal 704
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                    517 Val-----ProcysGlyThrPheThrPheGlnCysGlu---AspArgSerCysValLys
                                                                               -----GACACAGAAGACCAAGAAGACCAA-----
                                                                                                                                                               --GTAGATCCGCGCCTCATTGATGGGAAGATGACCAGGCGG
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                                                                                                                                                                                                                                                                                                                                                                   593 AlaLeuIleAlaAspArgTrpValIleThrAlaAlaHisCysPheGlnGluAspSerMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                       613 AlaSerProLysLeuTrpThrValPheLeuGlyLys-----MetArgGlnAsnSerArg
                                                                                                                                                                                                                                                                                                                            GTGCTCATCCACCCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 70.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1171 GGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATC 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            782 GlyValTyrThrArgValThrArgVallleAsnTrpIle 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           653 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                 469 CGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBVCS4;
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                                                                                                                                                                 964
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43 CGGGAGTGCATAGAGGAGATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTG 102
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192 LysAspCysGlyThrGluLysCys---PheAspGluThrArgTyrGluTyrPheGluVal 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 GATGACACACTGGCCTTCTGGTCCAAGCACGTCGACGGT-----GACCAGTGCTTGGTC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 TGGGGGACGGCACGTGC----ATCGACGCATCGGCAGCTTCAGCTGCGACTGCCGC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 TIGCCCTIGGAGCACCCGIGC------------GCCAGCCIGTGC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 GlyAsp------HisTrpAlaArgValSerGluGlyHisValGluGlnCysGlyCys 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 LeuAsnGlyGlyThrCysHisLeuILeValGlyThrGlyThrSerValCysThrCysPro 267
                                                               to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70553 MW; FE18D90174ED6FDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        653
136
67
166
119
19
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                              PRINTED PRODOMY PROPORTE; PROJECT 1.

SMART; SMOODES; FNL; 1.

SMART; SMOODES; FNL; 1.

SMART; SMOODES; FNL; 1.

SMART; SMOODES; FNL; 1.

PROSITE; PSOODES; EGE_1; UNKNOWN_1.

PROSITE; PSOODES; FIRENDECTIN_1; UNKNOWN_1.

PROSITE; PSOODES; FIRENDECTIN_2; UNKNOWN_1.

PROSITE; PSOODES; FIRENDECTIN_2; UNKNOWN_1.

PROSITE; PSOODES; FIRENDECTIN_2; UNKNOWN_1.

PROSITE; PSOODES; TRYPSIN_DOM; 1.

PROSITE; PSOOLES; TRYPSIN_DOM; 1.

PROSITE; PSOOLES; TRYPSIN_LIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                       InterPro; IPR000742; EGE_2.
InterPro; IPR001438; EGF_II.
InterPro; IPR001083; Flbrncfnl.
InterPro; IPR000562; FN_Type_II.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-763-153-1 (1-1245) x Q8VCS4 (1-653)
                                             Strausberg R.;
Submitted (DEC-2001) to the EMBL/Ge
BMEL; BC019376, AAH19376.1;
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                          Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00013; FNTYPEII.
PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.49e-26
477.50
41.60%
27.87%
                                                                                                                                                                                                             Pfam; PF00008; EGF; 2
Pfam; PF00039; fn1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al protein.
653 AA; 7
                                                                                                                                                                                                                                               PF00040; fn2;
[1]
SEQUENCE FROM N.A.
TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
SEQUENCE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                              Pfam;
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309

244 AGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTGGAC 303

Db 287	AsnGlyThrGluTyrArgGlyValAlaSerThrAlaAlaSerGlyLeuSerCysLeuAla	306
309		309
307	TrpAsnSerAspLeuLeuTyrGlnGluLeuHisValAspSerValAlaAlaAlaValLeu	326
310		330
327		346
m	GAGGAGGTGGCGGCGGCGGTGTAGC 3	357
347	TyrValValLysAspAsnAlaLeuSerTrpGluTyrCysArgLeuThrAlaCysGluSer 3	366
358	TGTGCGCCTGGCTACAAGCTGGGGGACCTCCTGCAGTGTCACCCC 4	405
367	LeuAlaArgValHisSerGlnSerProGluIleLeuAlaAlaLeuProGluSerAlaPro	386
406	GCAGTGAAGTTCCCTTGTGGGAGGCCCTGGAAGCGGATGGAGAAGAGCGCAGTCACCTG 4	465
387	AlavalArgProThrCysGlyLysArgHisLysArgThrPheLeu 4	102
466	AAACGAGACACAGAAGACCAAGAAGACCAAGTAGATCGGGGCTCATTGATGGGAAGATG 5	525
403	Arg	111
526	ACCAGGCGGGAGACAGCCCCTGGCAGGTGGTCCTGGTGGACTCAAAGAAGAAGCTGGCC 5	585
412	::: SerLeuProGlySerHisProTrpLeuAlaAlaIleTyrIleGlyAsnSerPhe	429
586	TGCGGGGCAGTGCTCATCCACCCCTCCTGGGTGCTGACAGCGGCCGACTGCATGAG	645
430		149
646 450	TCCAAGAAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGGCGCGGGAG 6	969
697	AAGTGGGAGCTGGACCTGGACATCAAGGAGGTCTTCGTCCACCCCAACTACAGGAAGAGC 7	,56
470	AspvalThrGlnThrPheGlyIleGluLysTyrValProTyrThrLeuTyrSerValPhe 4	189
757	ACCACCACAAT GACATCGCACTGCTGCACCTGGCCCAGCCCGCC 8	303
490	AsnProAsnAsnHisAspLeuValLeuIleArgLeuLysLysClyGluArgCysAla 5	609
802	ACCUTICGCAGACCATAGTGCCCATCTGCCTCCCGGACGCGCCTTGCAGAGCGCGAG 8	191
510	ValArgSerGlnPheValGlnProlleCysLeuProGluAlaGlySerSer 5	97
862	CICAAICAGGCGGGCGAGGAGCCCTGGTGACGGGCTGGGGCTACCACAGCAGCGAGAG 9	121
527	nVal 5	4 5
922	CATCAAGATTCCCGTGGTCCCG 9	181
546	lAla 5	19
982	CACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCTGAGAACATGCTGTT 1C	035
562	sserSerProGluValTyrGlyAlaAspIleSerProAsnMetLeuCys 5	81
1036	CGAGGGCGACAGTGGGGGGCCCCATGGTC 1	095
582	 PheAspCysLysSerAspAlaCysGlnGlyAspSerGlyGlyProLeuVal 6	01
0 0	STCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGGGGTGAGGCTGTGGGG 1	-
9	sıdıysasndıyvalalaryrlediyrdiylleileserTrpGlyaspGlyCysGly 6	21
1156	CTCCTTCACAACTACGGGGTTTACACCAAAGTCAGCGGCTACCTGGACTGGATGGG 12	215

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RX MEDLINE=2108560; PubMed=11217851;
RX MEDLINE=2108560; PubMed=11217851;
RAWal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salto T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Balalov S., Casavant T.,
RA Kadota K., Matsud H.A., Saburner M., Balalov S., Casavant T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
Ructional annotation of a full-length mouse cDNA collection.";
CC '-- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
622 ArgieuAsniysProGlyValTyrThrArgValAlaAsnTyrValAspTrplleAsnAsp 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
130015B06Rik protein.
                                                                                                                                                                                                                                                                                         399 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SMOODS, GLA: 1.
SMART; SMOODS, Tryp.SPc; 1.
PROSITE; PSO0010; ASX_HYDROXYL; UNKNOWN_1.
PROSITE; PS01022; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLU_CARBOXYLATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000742; EGF 2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR0012883; GIA_blood,
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR000294; Vitk_dep_GLA.
                                                                   1216 CACATCAGAGACAAGGAAGCCCCC 1239
                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                       642 ArglleArgProProLysArgPro 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD, MGI:1914151; 1300015B06R1k.
InterPro; IPR000152; Asx. hydroxyl.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000561; EGF-11ke.
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PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS, PR00722; CHYMOTRYBSIN.
PRINTS, PR00001; GLABLOOD.
SMART; SM00101; EGF; 2.
SMART; SM00179; EGF_CA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00594; gla; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00008; EGF; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1300015B06RIK.
                                                                                                                                                                                                                                                                                                              09CQW3;
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70 ITCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGGATGACACACTGGCCTTCTGGTCCAAG 129
                                                                                                                                                                                                                                                                                                                                                                     130 CACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGCGCCAGCCTGTGC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                             190 TGCGGGCACGCACGTGCATCGACGCATCGGCAGCTTCAGCTGCGAACTGCCGCAGCGGC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 LeuAsnAsnGlyThrCysGluAspHisIleArgSerTyrSerCysThrCysSerProGly 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 reggaegececticieccaececagegergacticctcaattectegetegac---aac 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::||||||::: |||
117 TyrGluGlyLysThrCysAlaMetAlaLysAsn-----GluCysHisLeuGluArgThr 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 GGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGCTGTAGCTGTGCGCCT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 AspGlyCysGlnHisPheCysHisProGlyGlnSerSerTyrMetCysSerCysAlaLys 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 GGCTACAAGCIGGGGACGACCICCTGCAGIGICACCCGGCAGIGAAGIICCCTIGIGGG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             427 AGGCCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGACACAGAGACAA 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      487 GAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGGGGAGACAGC--- 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 ------AlaLeuThrSerGluHisIle-------181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 ProSerPheProTrpGlnValArgLeuThrAsnSerGluGlyGluAspPheCysAlaGly 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 TICCIGGAGGAGCICCGICACAGCAGCCTGGAGCGGGAGTGCAIAGAGGAGAICIGIGAC 69
                                                                                                                                                                                                                                          65 TyrGluGluAlaArgGluValPheGluAsnAspValIleThrAspGluPheTrpArgGln 84
                                                                                                                                                                                                                                                                                                                                                                                                          85 TyrdlyglyglyserProCysValSerGlnPro-------------------------Cys 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             655 CTCCTTGTCAGGCTTGGAGAGTATGACCTGCGGCGCTGGGAGAAGTGGGAGCTGGACCTG 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     595 GTGCTCATCCACCCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAG 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 IleSerValLys---AlaAsnValAspGlnArg------------------1le 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     715 GACATCAAGGAGGTCTTCGTCCACCCCAACTACAGCAAGAGCACCACCGACAATGACATC 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 ArgileLysSerThrHisValHisMetArgTyrAspGluGluSerGlyGluAsnAspVal 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            775 GCACTGCTGCACCTGGCCCAGCCCGCCACCTCTCGCAGACCATAGTGCCCCATCTGCCTC 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 SerLeuLeuGlnLeuGluProLeuGlnCysProSerSerGlyLeuProValCysVal 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 ProGluArgAspPheAlaGluHisValLeu---IleProGlyThrGluGlyLeuLeuser 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    895 GGCTGGGGCTACCACAGCAGCGAGAGAAGGAGGCCAAGAAAACCGCACCTTCGTCCTC 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               544 ------CCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGATGGCCTGCGGGGCA
   4FC85C9598F27E03 CRC64;
                                                            399
126
58
58
143
16
                                                                                               Conservative:
                                                                                                                 Mismatches:
                                                                              Matches:
                                                                                                                                Indels:
                                                            Length:
                                                                                                                                                    Gaps:
                                                                                                                                                                               US-09-763-153-1 (1-1245) x Q9CQW3 (1-399)
399 AA; 44304 MW;
                                                      4.85e-26
470.00
43.71%
29.93%
20.11%
                                                                                                             Best Local Similarity:
                                                                                         Percent Similarity:
                                     Alignment Scores:
 SEQUENCE
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RAINTENEMELELS.

RAMINEDELINE—20196006; PubMed=10731132;

RADAMEN D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Scherer S.E., Ii P.W., Hoskins R.A., Galle R.F.,

RA Gorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandreal M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Pfeififer B.D.,

RA Man K.H., Doyle C., Baxerer B.G., Hell G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baslawin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Basaley E.M.,

Ballew R.M., Cawley S., Derman B.P., Bhandrai D., Boslakov S.,

Borkova D., Botchan M.R., Buuke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Fosler C., Gabrielian A.E., Garrel J.H., Gu Z., Glan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J., Matkei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mosherson D.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Nalson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

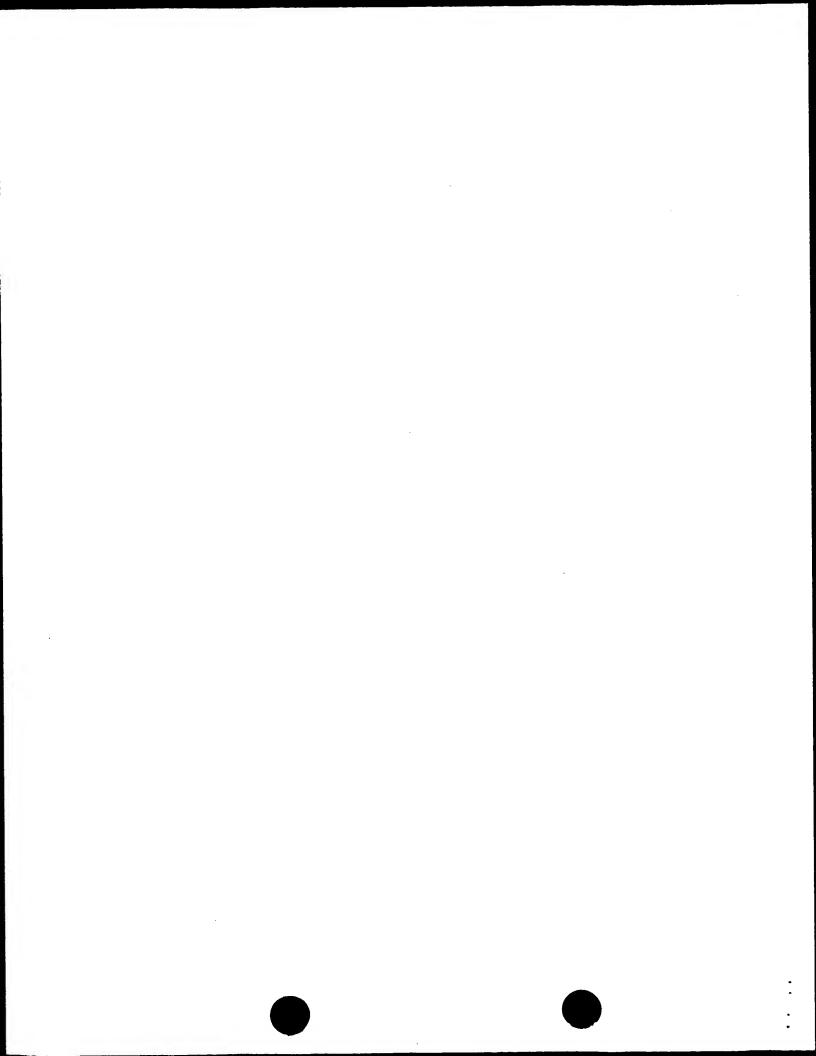
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 1144 GAGGGCTGTGGGCTCCTTCACAACTACGGCGTTTACACCAAAGTCAGCCGCTACCTCGAC 1203
                                                                                                                                                                                                                                            1039 GGCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGCGACAGTGGGGGGCCCATGGTCGCC 1098
                                                                                                                                                                                                                                                                                                                                        1099 ICCITCCAC---GGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGG-------GGT 1143
                                                                                                                                                  988 GAGTGCAGCGAGGTCATGAGCAACATGGTGTCTGAGAACATGCTGTGT------GCG 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                 345 ValValMetGlyProTrpValGlu---------GlySerValValThr 357
                                                                                                   305 AsnGlyThrHisLeuAlaThrThrProMetLeuLeuSerValThrGlnAlaAspGlyGlu 324
         ------304
                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly)
                   301 GlyTrp------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7227;
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906 GluTyrValCysAspGlyHisLeuAspCysMetAspGlnAlaAspGluAlaLysCysGlu 925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              926 ArgCysGlyProAspGluIleTyrCysGlyAspSerGlnCysIleGlyThrLySHisIle 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   946 CysAsp61y11e-----IleAspCysProTyrGlyGlnAspGluArgAsnCys 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 CAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTGCACACGGCGGCTGCACGCATTACTGC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 GCCTTCTGGTCCAAGCACGTCGACGGTGACCAGTGC-----TTGGTCTTGCCCTTG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       886 AlaalaThrHisProLysCysAspGlyPheGlnCysAspGlnAsnArgCysLeuProGln 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 GAGGAGATCTGTGACTTCGAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTG 114
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Williams S.M., Rodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Zheng X.H., Zhong F.N., Zhon M., Zhan G., Zhu S., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.; Schoos Sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Hydrolase; Serine protease.
SEQUENCE 1379 AA; 149489 MW; A593A9CC2167E4B7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                  InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000024; Fz_domain.
InterPro; IPR001212; LDL_recept_A.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR001199; Srcr_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-763-153-1 (1-1245) x Q9V4N6 (1-1379)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50038; FZ; 1.
PROSITE; PS50038; FZ; 1.
PROSITE; PS50068; LDLRA_1; 1.
PROSITE; PS50048; SRCR_2; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50134; TRYPSIN_LIS; 1.
PROSITE; PS00134; TRYPSIN_LIS; 1.
PROSITE; PS00135; TRYPSIN_LIS; 1.
                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01392; Fz; 1.
Pfam; PF01392; Fz; 1.
Pfam; PF00089; Tryps.n. 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00261; LDLRECEPTOR.
SNART; SM00061; FRI; 1.
SNART; SM00202; SR; 1.
SNART; SM00202; SR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 GAGCACCCGTGC------
                                                                                                                                                                                                                    EMBL, AE003840; AAF59230.1; -. HSSP; P00763; 1DPO. Flybase; Fbgn0033192; CG2105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.34e-24
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39.76%
26.98%
18.85%
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                                                                                                                                                                                                           TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
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QQ	962	LeuArgLeuSerGluArgAsnGlyAspValGlyThrGlyValLeuGluValTyrArg 980
٥y	328	CTAGAGGAGGTGGGCGGCGCTGT
QQ	981	::: ::: IleGlyGlnArpMetProAlaCysValLysAsnTrpAspArgAlaValSer 999
QY	376	CTGGGGGACGACCTCCTGCAGTGACCCCCGCAGTGAAG 414
qq	1000	::: ProSerAlaValCysSerIleLeuGlyTyrSerAlaValAsnAlaThrSerValLeuThr 1019
οy	415	TTCCCTTGTGGGAGGCCCTGGAAGCGG 441
qq ,	1020	GlnLeuThrH1sArgProLeuLeuAlaThrValAsnValSerThrAspIleTrpLysMet 1039
	1040	ATGGAGAAGAAGCGCAGTCACCTGAAACGAGACACAGAAGAC 483             TyralaLysArgLysSerThrLeumetGlnGluPhealaAsnCvsLysLysThrGluAsp 1059
à	484	GAA
q	1060	TyrProMetAlaAspieuThrCysSerAsnTyrGluCysGlyArgValLysArgGlyArg 1079
λά	490	GACCAAGTAGATCCGCGCCTCATTGATGGGAAGATGACCAGGCGGGGAGACAGCCCCTGG 549
අ	1080	HisLysProSerArgArgIleIleGlyGlyThrGlnAlaSerProGlyAsnTrpProPhe 1099
λζ	550	CAGGIGGICCTGCTGGACTCAAGAAGAAGTGGCCTGCGGGGCAGTGCTCAC 606
අ	1100	LeuAlaAlaIleLeuGlyGlyProGluLysIlePheTyrCysAlaGlyValLeuIleSer 1119
ζŽ	607	CCCTCCTGGGTGCTGACAGCGGCCCACTGCATGATGAGTCCAAGAAGCTCCTTGTCAGG 666
g	1120	AspGlnTrpValLeuThrAlaSerHisCys1129
λχ	299	CTTGGAGAGTAFGACCTGCGGCGCTGGGAGAGTGGGACCTGGACCTG 714
q	1130	ValGlyAsnTyrSerVallleAspLeuGluAspTrpThrIleGlnLeuGlyValThrArg 1149
ζ	715	GACATCATCGAGGTCTTCGTCCACC 741
ą	1150	ArgasnSerPheThrTyrSerGlyGlnLysValLysValLysAlaValIleProHisPro 1169
λ.	742	AACTACAGCAAGAGCACCACCGACAATGACATCGCACTGCTGCTGCCTGGCCCAGCCC 798
q,	1170	GlnTyrAsnMetAlaIleAlaHisAspAsnAspIleAlaLeubheGlnLeuAlaThrArg 1189
,	799	GCCACCCTCTCGCAGACCATAGTGCCCCATCTGCCTCCGGGACAGCGGCCTTGCAGAGCGC 858
2	1190	valAlaPheHisGluHisLeuLeuProValCysLeuProProSerValArg 1207
λ	859	GAGCTCAATCAGGCCGGGCCAGGAGACCCTCGTGACGGGGTGGGGGTACCACAGCAGCCGA 918
q	1208	AsnleuHisProGlyThrLeuCysThrVallleGlyTrpGlyLysArgGlu 1224
λ	919	GAGAAGGAGGCCAAGAAACCGCACCTTCGTCCTAACTTCATCAAGATTCCCGTGGTC 978
ą	1225	AspLysAspProLysSerThrTyrGluTyrIleValAsnGluValGlnValProllelle 1244
Δi	979	CCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCTGAGAACATGCTGTGT 1035
q	1245	ThrArgAsnGlnCysAspGluTrpLeuAspAsnLeuThrValSerGluGlyMetValCys 1264
<u>۲</u> ۶	1036	GCGGGCATCTCGGGGACCGGCAGGATGCCTGCGAGGCGCAATGGTC 1095
3	071	AldelyFneAspAspelyGlyLysAspAlaCysGlnGlyAspSerGlyGlyProLeuLeu 1284
<u>ک</u> ۾	1096	GCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGGGGTGAG 1146
<u>&gt;</u>	1147	
. D	1305	MELCYSTALISTOP TO THE TRANSPORT OF THE STATE

Search completed: March 17, 2003, 17:35:20 Job time: 95.5 secs



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Command line parameters:
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-DE-ISSUEG_PARTIS_AA - QFWT-fastan - SUFFIX=N2P, rai - MINNATCH=0.1 - LOOPCL=0
-LOOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANNS-human40.cdi
-LIST=60 - DOCALIGN=200 - THR_SCORE=-DCt - THR_MAX=100 - THR_MIN-0 - ALIGN=20
-MODE-LOCAL - OUTFMT-PEC - NORM-ext - HEAPSIZE=500 - MINLEN=0 - RAXLEN=200000000
-USER=V0SO9753153 (CGNL 1_1_2] eTunat _ 11032003 084248_2035 - NCPU=6 - ICPU=3
-NO_XIPXY - NO_MMAP - LARGEQUERY - NEG_SCORES=0 - WAIT - LONGLOG - DEV_ITIMEOUT=120
-WARN_ITIMEOUT=30 - THREADS=1 - XGAPOF=10 - XGAPOFT=0.5 - FGAPOP=6 - FGAPOEXT=7
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1927.976 Million cell updates/sec
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                           using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 60 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5
7.0
7.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                        OM nucleic - protein search,
                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
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                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Ouery

No. Score Match Length DB ID

2 2298 98.3 419 2 US-08-955-471-1 Sequence 1, Appli 2 2298 98.3 419 4 US-09-667-570A-3 Sequence 1, Appli 5 2298 98.3 460 2 US-08-955-471-1 Sequence 1, Appli 5 2298 98.3 460 2 US-08-955-471-1 Sequence 1, Appli 6 2298 98.3 460 2 US-08-756-506-4 Sequence 2, Appli 7 2298 98.3 460 2 US-08-756-506-4 Sequence 2, Appli 8 2292 98.1 461 6 5270178-17 Patent No. 522537 Patent No. 5270178-17 Patent No. 527

Sequence 1, Appli Sequence 1, Appli	0. 527017	e 2. Apple	NO.	0. 527017	Sequence 1, Appl	NO. 527017	Sequence 51, App	atent No. 527017	: No. 527017	ence 53, App	equence 53, App	equence 2, Appl	2, Appl	equence 1, Appl	equence 3. Appl	3, Appl	equence 5, Appl	equence 5, Appl	equence 5,	2, Appl	equence 2, Appl	equence 2,	equence 2, Appl	ednence 2,	equence 2, Appl	equence 2, Appl	equence 2,	equence 2, Appl	equence 4.	4, Appl	14,	14, App	4, Appl	7,	1,	5,	quence 1, Appl	tent No. 552107	equence 2, Appl	eguenc	equence 3, Appl	equence 2, Appl.
4 US-09-065-872-1 4 US-09-667-570A-1	5270178-2	US-09-667-570	5270178-15	97-8/10/75	5270178	5270178-2	US-08-944	5270178-2	5270178-5	US-08-469-486-	US-08-469-658-5	US-08-469-486-	- 403-603-009-008-	US-08-295-411-3	US-08-955-471-	PCT-US92-10242	US-08-295-411-5	US-08-955-471-5	PCT-US92-10242	US-08-475-845-2	US-08-327-690-	US-08-660-289-	US-08-537-807-	US-08-871-003-	US-08-464-233-	-/09-68T-60-SD	2-106-916-60-50 -02230-400-02230	US-07-882-2024	US-08-021-	US-08-321-777-4	US-09-009-217-1	US-09-009-626-1	PCT-US93-04493	US-08-073-531B-	US-08-766-288-	US-08-487-	US-08-487-037-	5521070-2	US-08-742-877-2	0-60-SD	US-08-487-037	US-08-295-411
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ALIGNMENTS

RESULT 1

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US-08-295-411-1

Sequence 1, Application US/08295411

Sequence 1, Application US/08295411

Sequence 1, Application US/08295411

Sequence 1, Sequence 1, Settlein, John H.

APPLICANT: Trillin, John H.

APPLICANT: Mesters Rolf M.

TITLE OF INVENTION: Serine Protease-Derived Polypeptides and Therapeutic Methods TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods TITLE OF INVENTION: for Inhibiting Coagulation

NUMBER OF SEQUENCES: 10

CORRESSEE: Office of Patent Counsel, The Scripps

ADDRESSEE: Office of Patent Counsel, The Scripps

ADDRESSEE: Office of Patent Counsel, The Scripps

CITY: La Jolla

STREET: 1066 No. 5679639th Torrey Pines Road, TPC 8

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

MEDIUM TYPE: Floppy disk
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121 TGGTCCAAGCACGTCGACGGTGACCAGTGCTTGGTCTTGCCCTTGGAGCACCCGTGGGCCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Protein C Activation
                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/295,411
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                        NAME: FILLING, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI263.0C1
TELECOMMUNICATION INFORMATION:
TELEPAN: 619-554-2937
TELEFAR: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                            PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                              APPLING DATE: 22-AUG-1994
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide"
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MOLECULE TYPE: protein
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OTHER INFORMATION:
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                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
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John H.
Rolf M.
Serine Protease-Derived Polypeptides and
Anti-Peptide Antibodies, Systems and Therapeutic Methods
for Inhibiting Coagulation
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                         421 TGTGGGAGGCCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGACACAGAA
                                                                                                                                  GACCAAGAAGACCAAGTAGATCCGCGCCTCATTGATGGGAAGATGACCAGGCGGGGAGAC
                                                                                                                                               541 AGCCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGCTGGCCGGGGCAGTGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08955471
Patent No. 5968751
GENERAL INFORMATION:
APPLICANT: GELIFIN, John H.
APPLICANT: MESTERS, Rolf M.
TITLE OF INVENTION: Serine Proteas
TITLE OF INVENTION: Anti-Peptide A
TITLE OF INVENTION: Tor Inhibiting
NUMBER OF SEQUENCES: 10
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                                    œ
      ADDRESSEE: Office of Patent Counsel, The Scripps ADDRESSEE: Research Institute STREET: 10666 No. 5968751th Torrey Pines Road, TPC CITY: La Jolla STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419
415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Protein C Light Chain'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Protein C Activation
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-763-153-1 (1-1245) x US-08-955-471-1 (1-419)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                          NAME: Fitting, Thomas
REISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSR1263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                         APPLICATION NUMBER: US/08/955,471 FILLING DATE:
                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide"
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2298.00
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98.33%
                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: /
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OTHER INFORMATION:
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LOCATION: 170..419
OTHER INFORMATION:
US-08-955-471-1
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                                                                                                                                                                                                CLASSIFICATION:
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Best Local Similarity:
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                                                                        USA
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                                                                       COUNTRY: US
ZIP: 92037
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baker, Jeffrey C
APPLICANT: Carlson, Andrew D
APPLICANT: Huang, Lihua
APPLICANT: Sheliga, Theodore A
APPLICANT: Sheliga, Theodore A
APPLICANT: Sheliga, Theodore A
APPLICANT: Sheliga, Theodore A
CURRENT SEFERENCE: X-11796A
CURRENT APPLICATION NUMBER: US/09/667,570A
CURRENT FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: 60/045,255
PRIOR PILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 3
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Matches:
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Sequence 3, Application US/09667570A Patent No. 6436397
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Anti-Peptide Antibodies, Systems and Therapeutic Methods
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ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
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APPLICATION NUMBER: PCT/US92/10242
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SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: U
FILING DATE: 18-NOV-1
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APPLICANT: Cottingham, Ian R.
APPLICANT: Temperley, Simon M.
APPLICANT: Foster, Donald C.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna E.
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1201 Eastlake Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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Peptide"
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Matches:
Conservative:
Mismatches:
Indels:
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                                         SCR0472P
           NAME: Fitting, Thomas
REGISTATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRO.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEPHONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            3.34e-167
2298.00
100.00%
100.00%
98.33%
 ATTORNEY/AGENT INFORMATION:
                                                                                                                       : 419 amino acids
AMINO ACID
                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                       LOCATION: 158..169
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Region
LOCATION: 170..419
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
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Best Local Similarity:
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ANTI-SENSE: N
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                                                                                                                                     TYPE:
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961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTTT 1020
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                                              ATCCACCCCTCCTGGGTGCTGACAGCGGCCCCACTGCATGGATGAGTCCAAGAAGCTCCTT
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                        OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                               APPLICATION NUMBER: US/08/756,506
                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARATERISTICS:
          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                  3.42e-167
2298.00
100.00%
100.00%
98.33%
Floppy disk
                                                                                                                                                                                                                       LENGTH: 460 amino acids TYPE: amino acid
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08-756-506-2
                                                                            FILING DATE:
CLASSIFICATION: 800
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Best Local Similarity:
Query Match:
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               243 IleHisproSerTrpValLeuThrAlaAlaHisCysMetAspGluSerLysLysLeuLeu
601 ATCCACCCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: ZymoGenetics, Inc.
1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/756,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Cottingham, Ian R.
APPLICANT: Femperley, Simon M.
APPLICANT: Foster, Donald C.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna E.
TITLE OF INVENTION: PROPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 4, Application US/08756506
; Patent No. 5905185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
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CITY: Seattle
STATE: WA
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US-08-756-506-4
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Mismatches:
Indels:
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                                                                                                                                                                      Length:
Matches:
      NAME: SAWISLAK, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKEY NUMBER: 95-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFRAX: 206-442-6672
                                                                                                                                                                  3.42e-167
2298.00
100.008
100.008
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                                                                       INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
                                                                                            LENGTH: 460 amino acids TYPE: amino acid
                                                                                                                           MOLECULE TYPE: protein
08-756-506-4
                                                                                                                  linear
                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                          gnment Scores:
                                                                                                                  TOPOLOGY:
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APPLICATION NUMBER: US/07/459,082
FILING DATE: 29-DEC-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Patent No. 5225537
; APPLICANT: FOSTER, DONALD
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Best Local Similarity:
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5460953-3
; Patent No. 5460953
APPLICANT: GERLITZ, BRUCE E.; GRINNELL, BRIAN W.
TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION GGLYCOSYLATION MUTANTS OF HUMAN PROTEIN C
NUMBER OF SEQUENCES: 3
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Mismatches:
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                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/93,217
FILING DATE: 09-SEP-1993
FILING DATE: 09-SEP-1993
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: 628,063
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: 484,081
FILING DATE: 23-FEB-1990
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99.76%
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APPLICANT: GERLITZ, BRUCE E.; GRINNELL, BRIAN W.
TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION SINGER FORMS OF HUMAN PROTEIN C
NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/484,133 FILING DATE: 23-FEB-1990
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Matches:
Conservative:
                                APPLICANT: GERLITZ, BRUCE E.;GRINNELL, BRIAN W
TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR
FYMOGEN FORMS OF HUMAN PROTEIN C
NUMBER OF SEQUENCES: 21
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Indels:
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                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/484,133
FILING DATE: 23-FEB-1990
                                                                                                                                                                     9.29e-165
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99.28%
98.55%
96.96%
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Best Local Similarit
                     ;Patent No. 5270178
                                                                                                                           LENGTH: 461
                                                                                                                                                           Alignment Scores:
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RESULT 10
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APPLICANT: GERLITZ, BRUCE E.;GRINNELL, BRIAN W.

TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
                                                                                                                                                                                                                                                                                                                                                                                          460
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Matches:
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CURRENT APPLICATION DATA:
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                                          GCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCT 420
                                                                                                                             TGTGGGAGGCCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGAGACACAGAA 480
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301 GACAACGGCGGCTGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGGCGCTGTAGCTGT
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                             OF
         APPLICANT: GERLITZ, BRUCE E.;GRINNELL, BRIAN W.
TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION
;ZYMOGEN FORMS OF HUMAN PROTEIN C
NUMBER OF SEQUENCES: 21
                                                                                                                                                                        460
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                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/484,133
FILING DATE: 23-FEB-1990
                                                                                                                                                                    2.43e-164
2260.50
99.28%
98.55%
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5270178
                                                                                                                  ; LENGTH: 460
5270178-14
                                                                                                                                                                                                Percent Similarity:
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                                                                                                     ; SEQ ID NO:14:
                                                                                                                                                                                                                           Query Match:
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GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Carlson, Andrew D
APPLICANT: Carlson, Andrew D
APPLICANT: Huang, Lihua
APPLICANT: Sheliga, Theodore A
TITLE OF INVENTION: Improved Methods for Processing Activated Protein C
TITLE OF INVENTION: Improved Methods for Processing Activated Protein C
FILE REFERENCE: aPC process patent
CURRENT APPLICATION NUMBER: 60/045,872
CURRENT FILING DATE: 1998-04-24
EARLIER FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LINGTH: 410
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; Sequence 1, Application US/09065872
; Patent No. 6162629
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Best Local Similarity:
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9-065-872-1
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       61 IleaspGlyIleGlySerPheSerCysAspCysArgSerGlyIrpGluGlyArgPheCys
                                                                                CAGCGCGAGGTGAGCTTCCTCAATTGCTCGCTGGACAACGGCGGCTGCACGTTACTGC
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APPLICANT: Baker, Jeffrey C
APPLICANT: Baker, Jeffrey C
APPLICANT: Carlson, Andrew D
APPLICANT: Huang, Lihua
APPLICANT: Huang, Lihua
APPLICANT: Sheliga, Theodore A
TITLE OF INVENTION: Improved Methods for Processing Activated Protein C
TITLE OF INVENTION: UNMBER: US/09/667,570A
CURRENT FILING DATE: 2000-09-21
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 3
SCOTTANE: Patentin version 3.1
: SEQ ID NO 1
: LENGTH: 410
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ORGANISM: Homo sapiens
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Query Match:
                                                                                                    GENERAL INFORMATION:
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Pred. No.:
Score:
                                                             US-09-667-570A-1
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US-09-667-570A-1
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                                              GCCCACTGCATGGATGAGTCCAAGAAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGG
                                                                       AlaHisCysMetAspGluSerLysLysLeuLeuValArgLeuGlyGluTyrAspLeuArg
                                                                                                                                            AGCAAGAGCACCACCGACAATGACATCGCACTGCTGCACCTGGCCCAGCCCGCCACCTTC
                                                                                             CGCTGGGAGAAGTGGGAGCTGGACCTGGACATCAAGGAGGTCTTCGTCCACCCCAACTAC
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Patent No. 5270178

APPLICANT: GERLITZ, BRUCE E.; GRINNELL, BRIAN W.

TILLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF

ZIMOGEN FORMS OF HOMAN PROTEIN C.

NUMBER OF SEQUENCES: 21.
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APPLICATION NUMBER: US/07/484,133
FILING DATE: 23-FEB-1990
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APPLICANT: Baker, Jeffrey C
APPLICANT: Bater, Jeffrey C
APPLICANT: Bater, Jeffrey C
APPLICANT: Carlson, Andrew D
APPLICANT: Shaliga, Lihua
APPLICANT: Shaliga, Theodore A
TITLE OF INVENTION: Improved Methods for Processing Activated Protein of TITLE OF INVENTION: Improved Methods for Processing Activated Protein of TITLE OF TITLE APPLICATION NUMBER: US/09/065,872
CURRENT FILING DATE: 1998-04-24
EARLIER APPLICATION UNBER: 60/045,255
EARLIER PILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 2
                       402 GlyGlyProMetValAlaSerPheHisGlyThrTrpPheLeuValGlyLeuValSerTrp
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US-09-065-872-2
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Betent No. 6436397

GENERAL INFORMATION:
APPLICANT: Baker, Jeffrey C

APPLICANT: Baker, Jeffrey C

APPLICANT: Hung, Lihua

APPLICANT: Sheliga, Theodore A

TITLE OF INVENTION: Improved Methods for Processing Activated Protein C

CURRENT APPLICATION NUMBER: US/09/667,570A

CURRENT FILING DATE: 200-09-21

PRIOR APPLICATION NUMBER: 60/045,255

PRIOR PLING DATE: 1997-04-28
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TYPE: PRT
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TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION
;ZYMOGEN FORMS OF HUMAN PROTEIN C
NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/07/484,133
FILLING DATE: 23-FEB-1990
SEQ ID NO:16:
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                                                                                                                                                                              AGCCCCTGGCAGGTGCTGCTGGACTCAAAGAAGAAGAAGCTGGCGGGGGAGTGCTC
                                                                                                                    1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCCTGGAGCGGGGAGTGCATAGAGGAG
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                                  Conservative:
                                           Mismatches:
Indels:
          Length:
Matches:
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                 2218.50
98.078
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                                 Percent Similarity:
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Alignment Scores:
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APC POLYPEPTIDES AND ANTI-PEPTIDE ANTIBODIES, DIAGNOSTIC METHODS AND SYSTEMS FOR INHIBITING APC, AND THERAPEUTIC METHODS
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                                 961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCT 1020
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342 GlyTyrHisSerSerArgGluLysGluAlaLysArgAsnArgThrPheValLeuAsnPhe 361
                                                                                                                          402 GlyGlyProMetValAlaSerPheHisGlyThrTrpPheLeuValGlyLeuValSerTrp
                                                                                                         1021 GAGAACATGCTGTGTGCGGGCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGCGACAGT
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the PC heavy chain, the amino acid residue
which begin at position 158 and end at 419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Scripps Research Institute, Office of Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3366 No. 5279956th Torrey Pines Court, Suite 240
                                                                                                                                                                                                                                                                                                                        442 AsptrpileHisGlyHisIleArgAspLysGluAlaProGlnLys 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/720,189
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/07720189 Patent No. 5279956
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TELEPHONE: 619-554-2937
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        John H.
Rolf M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: APC
TITLE OF INVENTION: ANT
TITLE OF INVENTION: APC
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy (
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Counsel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Griffin, APPLICANT: Mesters,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION:
US-07-720-189-1
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LOCATION: 1..262
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                                                                                                                                                                    GCAGTGCTCATCCACCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAG 651
                                                                                                                                                                                                                                                                               ATCGCACTGCTGCACCTGGCCCAGCCCGCCACCTTCGCAGACCATAGTGCCCATCTGC 831
                                                                                                  | AspthrGluAspGlnGluAspGlnValAspProArgLeuIleAspGlyLysMetThrArg 20
                                                                                                                                       21 ArgGlyAspSerProTrpGlnValValLeuLeuAspSerLysLysLeuAlaCysGly 40
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Mismatches:
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Search completed: March 17, 2003, 17:38:42 Job time : 56 secs

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March 17, 2003, 17:35:25 ; Search time 47 Seconds (without alignments) 2441.899 Million cell updates/sec
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GenCore version 5.1.4_-p5_-4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                     OM nucleic - protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                             199416 seqs, 46092074 residues
                                                                                                                                                                                                                                                                                  0.5
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Maximum DB seq length: 200000000
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Command line parameters:

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-UB=Published\_Applications\_AA -QFMT=fastan -SUFFIX-ADp.rapb -MINMATCH=0.1
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-TRANS-human40.cdi -LIST=60 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100
-THR\_MINN-0 -ALIGN=-LOCAL -QUTFMT=ptc -NORM-ext -HEAPSIZE=500 -MINLEN=0
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-FGAFEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 60 summaries

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	14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Match I	98.3 98.3 98.3
Query Score Match Length DB ID	2298 2298 2298 2298
Result No.	4 3 5 1

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US-10-182-263-5 US-10-182-263-6 US-10-182-263-6 US-10-182-263-6 US-0-184-901-3 US-09-118-748-2 US-09-118-748-2 US-09-978-995-169 US-09-978-95A-16	US-09-999-8328-89-8328-89-8328-89-8328-80-898-6088-618-98-89-618-98-98-1-98-98-98-98-98-98-98-98-98-98-98-98-98-	US-09-788-142-1 US-09-761-120-1 US-09-808-602-10 US-09-808-602-10 US-09-9000-751-2 US-09-912-559-3 US-09-946-893-2 US-09-147-917-6 US-09-147-917-6 US-09-147-917-6 US-09-147-917-6 US-09-147-917-6 US-10-045-367-81-1	S-09-895-814-99 US-09-759-143-9 US-09-8780-669-9 S-10-012-896-93 S-09-895-793-93 S-09-895-793-93 S-09-759-143-9 US-09-780-669-9 US-09-780-669-9 US-09-133-23	09-895-793-8 109-895-814-8 109-759-143-8 109-780-669-8 109-879-9 100-09-82-827-9 100-099-700A-
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ALIGNMENTS

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APPLICANT: Jones, Bryan E
APPLICANT: Grinhell, Brian W
APPLICANT: Grinhell, Brian W
TILLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
                                                      Sequence 1, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: GERLItz, Bruce E
RESULT 1
US-10-182-263-1
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AAGGAGGTCTTCGTCCACCCCAACTACAGCAGAGCACCACCGACAATGACATCGCACTG 780
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Mismatches:
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Matches:
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PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
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2298.00
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                                                 SOFTWARE: Patentin version 3.1
                                      NUMBER OF SEQ ID NOS: 12
                                                                                                      ; ORGANISM: Homo sapiens
US-10-182-263-1
                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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                                                               SEQ ID NO 1
LENGTH: 419
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TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219u3310 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2011-10-17
NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                    1081 GGGGGCCCATGGTCGCCTCCTTCCACGCCACGGTTCCTGGTGGGCCTGGTGAGCTGG
                                                        841 AGCGGCCTTGCAGAGCGCGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGCTGG
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; Publication No. US20030027299A1
; GENERAL INFORMATION:
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Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 98.33%
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LENGTH: 419
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Mismatches:
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                                                 APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
                                                                                                       CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
                                                                                                                     CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
; Sequence 2, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
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                                                                                      661 GTCAGGCTTGGAGAGTATGACCTGCGCGCGGGAGAAGTGGGGAGCTGGACCTGGACATC 720
                                           Sequence 2, Application US/09978917A
Publication No. US20030027299A1
GENERAL INFORMATION:
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219us310 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
URRENT FILING DATE: 2001-10-17
CORRENT FILING DATE: 2001-10-17
CORRENT FILING DATE: 2001-10-17
                                                                           721 AAGGAGGTCTTCGTCCACCCCAACTACAGCAAGAGCACCACCGACAATGACATCGCACTG
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Best Local Similarity:
Query Match:
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US-09-763-153-1 (1-1245) x US-09-978-917A-2 (1-461)
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1081 GGGGGCCCATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGG 1140
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403 GlyGlyProMetValAlaSerPheHisGlyThrTrpPheLeuValGlyLeuValSerTrp 422
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APPLICANT: Grinnell, Brian W
TILLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
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NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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Query Match:
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APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
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Matches:
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PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
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                                                                     781 CIGCACCIGGCCCAGCCCACCCICTCGCAGACCATAGIGCCCAICIGCCTCCCGGAC
                                                                                                               901 GGCTACCACAGCAGCGAGAGAGAGAGGCCAAGAAACCGCACCTTCGTCCTCAACTTC
                                                      841 AGCGGCCTTGCAGAGCGCGAGCTCAATCAGGCCGGCCAGGAGACCCTCGTGACGGGCTGG
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Mismatches:
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APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR PLILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/181948
PRIOR PLILING DATE: 2000-03-14
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SOFTWARE: PatentIn version 3.1
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Mismatches:
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                                                                                                                                                   APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVARION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR PRILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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                                                                                        Sequence 4, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
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LENGTH: 419
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APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijina, Masabiko
TITLE OF INVENTION: With vesicle vector
TITLE OF INVENTION: with vesicle vector
FILE REFERENCE: 6627-F9A1170
CURRENT APPLICATION NUMBER: US/10/132,829
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/286,314
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              961 ATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTGTCT 1020
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                                                                                                     CTGCACCTGGCCCAGCCGCCACCTCTCGCAGACCATAGTGCCCATCTGCCTCCCGGAC 840
                                                                                                                                                                                                                                                                                                     GGCTACCACAGCAGCCGAGAGGAGGCCAAGAGAAACCGCACCTTCGTCCTCAACTTC 960
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                                            541 AGCCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGCTGGCCTGCGGGCAGTGCTC
                                                                                        ATCCACCCCTCCTGGGTGCTGACAGCGGCCCACTGCATGGATGAGTCCAAGAAGCTCCTT
                                                                                                                                                      GTCAGGCTTGGAGGTATGACCTGCGGCGCTGGGAGAAGTGGGAGCTGGACCTGGACATC
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blication No. US20030044982A1
ENERAL INFORMATION:
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APPLICANT: Miao, Carol
APPLICANT: Kay, Mark
TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use
                                    958 ITCATCAAGAITCCCGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATGGTG 1017
                                                                                            1018 TCTGAGAACATGCTGTGTGCGGGCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGGCGAC 1077
                                                                                                                                                       1078 AGTGGGGGGCCCATGGTCGCCTCCTTCCACGGCACCTGGTTCCTGGTGGGCCTGGTGAGC 1137
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                                                     :::371 TyrLeuArgValProLeuValAspArgAlaThrCysLeuArgSerThrLysPheThrIle 390
                                                                                                               --AlaLeuValLeuGln 370
                                                                                                                                                                                                                                 73 GAGGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACACTGGCCTTCTGGTCCAAGCAC 132
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Matches:
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CURRENT FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/212,902
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
    358 ArgValPheHisLysGlyArgSer----
                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09884901
Patent No. US20020076798A1
GENERAL INFORMATION:
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313 TGCACGCATTACTGCCTAGAGGAGGTGGGCTGGCGG---CGCTGTAGCTGTGCGCCTGGC 369
                                                                               370 TACAAGCTGGGGACGACCTCCTGCAGTGTCACCCCGCAGTGAAGTTCCCTTGTGGGAGG 429
                                                                                                         181 ValSerValSerGlnThrSerLysLeuThrArgAlaGluAlaValPheProAspValAsp 200
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                                                                                                                                                                                                                                                                                                                               502 -------CCGCGGCTCATTGATGGGAAGATGACCAGGCGGGGAGACAGCCCCTGG 549
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358 ArgValPheHisLysGlyArgSer-----
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US-09-118-748-2
; Sequence 2, Application US/09118748A
; Patent No. US20020031799A1
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Tue Mar 18 16:19:31 2003

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GENERAL INFORMATION:

APPLICANT: Stafford, Darrel W.

APPLICANT: Chang, Januare Current Application NUMBER: US/09/118,748A

CURRENT APPLICATION NUMBER: US/09/118,748A

CURRENT FILING DATE: 1997-07-17

EARLIER APPLICATION NUMBER: 60/053,571

EARLIER FILING DATE: 1997-07-21

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 CysGluGlnPheCysLysAsnSerAlaAspAsnLysValValCysSerCysThrGluGly 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 GluGluAlaArqGluValPheGluAsnThrGluArgThrThrGluPheTrpLysGlnTyr 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 CCCTGGAAGCGGATGGAGAAGAAGCGCAGTCACCTGAAACGA--
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Indels:
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Matches:
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1018 TCTGAGAACATGCTGTGCGGGCATCCTCGGGGACCGGCAGGATGCCTGCGAGGGCGAC 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 ArgValPheHisLysGlyArgSer-------AlaLeuValLeuGln 324
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                                                                                                                                                                                                                                                                                                                                                     294 GluTyrThrAsnIlePheLeuLysPheGly-----SerGlyTyrValSerGlyTrpGly 311
                                                                                                                                                                                                                                                                                                                                                                                             904 -----TACCACAGCAGCCGAGAGGAGGCCAAGAGAACCGCACCTICGTCCTCAAC 957
670 GGAGAGTATGACCTGCGCCTGGGAGAAGTGGGAGCTGGACCTGGACATCAAGGAGGTC 729
                                                                                                234 GlyGluHisAsnIleGluGluThrGluHisThrGluGlnLysArgAsnValIleArgIle 253
                                                                                                                                            730 ITCGICCACCCCAACIACAGCAAGAGCACCACC-----GACAAIGACAICGCACIGCIG 783
                                                                                                                                                                               254 IleProHisHisAsnTyrAsnAlaAla1leAsnLysTyrAsnHisAsp1leAlaLeuLeu 273
                                                                                                                                                                                                                                                     APPLICANT: Persson, Egon
TITLE OF INVENTION: Coagulation Factor VII Derivatives
FILE REFERENCE: 6286.200-10-22
CURRENT APPLICATION NUMBER: US/10/109,498
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 60/281,261
PRIOR PELICATION NUMBER: PA 2001 00477
PRIOR PILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-03-22
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SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: Xaa = Any Amino Acid
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ns-0	96	3-153-1 (1-1245) x US-10-109-498-1 (1-406)	
Qy Dp		1 GCCAACTCCTTCCTGGAGGAGCTCCGTCACAGCAGCTGGAGCGGGAGTGCATAGAGGAG 60	
Sp GS	61	ATCTGTGACTTCGAGGCCAAGGAAATTTTCCAAAATGTGGATGACACTGCCTTC 12	0
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d D	93	<pre>criddanawcgccgccTcCacgcaTtaCTgCcCTagaggaggTgggGcTgGcGgCcTgT 354 i::                                   </pre>	
Qy Dp	355 113	AGCTGTGGCCTGGCTAGAGCTGGGGGGAGCTCCTGCAGTGTACCCCGCAGTGAAG 4	
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QQ	133	:::         :: TyrProCysGlyLysIleProIleLeuGluLysArgAsnAla14	
ο <sub>γ</sub>	475	ACAGAAGACCAAGAAGACCAAGTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGG	
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δλ	652	AAGCTCCTTGTCAGGCTTGGAGAGTATGACCTGCGGCGCTGGGAGAAGTGGGGAG	
qq	201	TrpArgAsnLeulleAlaValLeuGlyGluHisAspLeuSerGluHisAspGlyAspGlu 22	
Oy Db	706	CIGGACCIGGACAICAAGGAGGICIICGICCACCCCAACIACAGCAAGAGCACCACGAC 765	
Qy	166	AATGACATCGCACTGCTGCACCTGGCCCAGCCGCCACCTCTCGCAGACCATGCTGCCC 82	
qq	241	:::	
Qy Dp	826 261		
Qy	886		
qq	280	LeuValSerGlyTrpGlyGlnLeuLeuAspArgGlyAlaThrAla 294	
Qy Db	946 295	TTCGTCCTCAACTTCATCAAGATTCCCGTGGTCCCGCACAATGAGTGCAGGAGGTCATG 100	ν

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1006 ------AGCAACATGGTGTCTGAGAACATGCTGTGTGCGGGCATCCTCGGG 1050
                                                                        1051 GACCGGCAGGATGCCTGCGAGGGCGACAGTGGGGGGCCCATGGTCGCCTCCTTCCACGGC 1110
                                                                                                                                                   1111 ACCTGGTTCCTGGTGGGCCTGGTGAGGTGAGGGCTGTGGGGCTCCTTCACAACTAC 1170
                                                                                                                                                                                                                             1171 GGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATCCATGGGCACATCAGAGACAAG 1230
                                                                                                335 GlySerLyssAspSerCysLysGlyAspSerGlyGlyProHisAlaThrHisTyrArgGly 354
                                                                                                                                                                         315 ArgLysValGlyAspSerProAsnIleThrGluTyrMetPheCysAlaGlyTyrSerAsp 334
                                                                                                                                                                                                                                                  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same File Reference: p2630plC11
CURRENT APPLICATION NUMBER: U5/09/978, 295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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Goddard, Audrey
Goddowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 169, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
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PRIOR PLILIG DATE: 2001-07-30
PRIOR PILING DATE: 1909-10-17
PRIOR PELLING DATE: 1909-10-17
PRIOR PELLING DATE: 1997-10-17
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PRIOR PELLING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/005364
PRIOR PELLING DATE: 1998-03-10
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
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Filvaroff, Ellen
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Botstein, David
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APPLICANT: Baker Kevin P
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PRIOR APPLICATION NUMBER: 60/080334
PRIOR PILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/08104
PRIOR APPLICATION NUMBER: 60/08104
PRIOR PILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/08105
PRIOR APPLICATION NUMBER: 60/08129
PRIOR FILING DATE: 1998-04-08
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PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-09 R FILING DATE: 1998-03-25
R APPLICATION NUMBER: 60/079656
R FILING DATE: 1998-03-26
R APPLICATION NUMBER: 60/079664
R FILING DATE: 1998-03-27
R APPLICATION NUMBER: 60/079689 PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-13
PRIOR FILING DATE: 1998-03-23
PRIOR PLING DATE: 1998-03-20
PRIOR PILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/078936
PRIOR APPLICATION NUMBER: 60/078936
PRIOR APPLING DATE: 1998-03-20
PRIOR APPLING DATE: 1998-03-20 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-21 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081819 FILING DATE: 1998-04-15 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081952 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081838 FILING DATE: 1998-03-31 APPLICATION UNMBER: 60/080107 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080165 FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079663
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APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/078939 FILING DATE: 1998-03-30 APPLICATION NUMBER: 60/079923 FILING DATE: 1998-03-30 APPLICATION NUMBER: 60/080105 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080194 APPLICATION NUMBER: 60/079786 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079920 APPLICATION NUMBER: 60/077649 APPLICATION NUMBER: 60/079294 FILING DATE: 1998-03-20 FILING DATE: 1998-03-1 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR

FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085580 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085573 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085700 APPLICATION NUMBER: 60/085323 FILING DATE: 1998-05-13 60/085579 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084643 APPLICATION NUMBER: 60/085339 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085582 APPLICATION NUMBER: 60/083500 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083742 FILING DATE: 1998-04-30 APPLICATION NUMBER: 60/084366 FILING DATE: 1998-05-05 APPLICATION NUMBER: 60/084441 FILING DATE: 1998-05-06 APPLICATION NUMBER: 60/084639 APPLICATION NUMBER: 60/084640 FILING DATE: 1998-05-07 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084600 APPLICATION NUMBER: 60/084627 60/085338 FILING DATE: 1998-04-22 APPLICATION UNBER: 60/082797 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082796 APPLICATION NUMBER: 60/083496 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083499 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083545 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083559 APPLICATION NUMBER: 60/084414 APPLICATION NUMBER: 60/084637 APPLICATION NUMBER: 60/084598 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082704 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082804 FILING DATE: 1998-04-23 APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-27 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083495 APPLICATION NUMBER: 60/083554 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083558 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082700 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083392 FILING DATE: 1998-05-15 FILING DATE: 1998-04-29 FILING DATE: 1998-05-07 FILING DATE: 1998-05-07 FILING DATE: 1998-04-29 FILING DATE: 1998-05-07 FILING DATE: 1998-05-1 FILING DATE: 1998-05-0 FILING DATE: 1998-05-1 FILING DATE: 1998-04-2 APPLICATION NUMBER: PRIOR I PRIOR PRIOR
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172 CCGTGCGCCAGC-----CTGTGCTGCGGGCACGGCACGTGCATC------GACGGC 216
                                                                                                                                                                                                                                                                                                                448 ProCysProGlyGluPheLeuCysSerValAsnGlyLeuCysValProAlaCysAspGly 467
                                                                                                                                                                                                                                                                                                                                                    217 ATCGGCAGCTTCAGCTGCGACTGCCGCAGCGGCTGGGAGGCCCGCTTCTGCCAGCGCGAG 276
                                                                                                                                                                                                                                                                                                                                                                           484 AlaThrPhe---GlnCysLysGluAspSer-----ThrCysIleSerLeuProLys 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 GTGGGCTGGCGCGCTGTAGCTGTGCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAG 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 TGTCACCCGCAGTGAAGTTCCCTTGTGGGAGGCCCTGGAAGCGGATGGAGAAGAAGCGC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            516 CysGlnGluGlyVal-----ProCysGlyThrPheThrPheGlnCysGlu---AspArg 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 SerCysVallysProAsnProGlnCysAapGlyArgProAspCysArgAspGlySer 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 GACCAAGAA------GACCAAGTAGATCCGCGGCTCATTGATGGGAAG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           553 AspGluGluHisCysAspCysGlyLeuGlnGlyProSerSerArglleValGlyGlyAla 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                523 ATGACCAGGCGGGAGACAGCCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGGCTG 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        697 ---AAGIGG-----GAGCIGGACCIGGACAICAAGGAGGICTICGICCACCCCAACIAC 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  748 AGCAAGACCCACCGACAATGACATCGCACTGCTGGACCTGGCCCAGCCCGCCACCTC 807
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
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PRIOR APPLICATION NUMBER: 60/085697
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988 GAGTGCAGCGAGGTCATGAGCAACATGGTGTGTGAGAACATGCTGTGTGCGGGCATCCTC 1047
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                                                                                                                                                                                                             1105 CACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGAGGTGAGGCTGTGGGCTTCTCAC 1164
                                                                  743 LysGlyLysLysAspAlaCysGlnGlyAspSerGlyGlyFroLeuValCysLysAlaLeu 762
706 ProlleSerAsn-----AlaLeuGlnLysValAspValGlnLeuIleProGlnAsp 722
                                                                                                                                                                                                                                        TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                  1165 AACTACGGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATC 1209
                                                                                                                                                                                                                                                                                                                      783 TyrPhedlyValTyrThrArgileThrGlyVallieSerTrplle 797
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CURRENT APPLICATION NUMBER: US/09/978,697
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1997-10-17
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PRIOR PELING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06314
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-21
PRIOR PELING DATE: 1997-11-21
PRIOR PELING DATE: 1998-03-10
PRIOR PELING DATE: 1998-03-11
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Patent No. US20020169284A1
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Gurney, Austin L.
Hillan, Kenneth J
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Roy, Margaret Ann
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Filvaroff, Ellen
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Kuo, Sophia S.
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Botstein, David
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Pan, James;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumas, Daniel
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RICH FILING DATE: 1998-04-08
RICH RELING DATE: 1998-04-08
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PRICH RELING DATE: 1998-04-09
PRICH APPLICATION NUMBER: 60/08125
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DR FILING DATE: 1998-04-01
DR FILING DATE: 1998-04-08
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R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080107
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R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/080328
R APPLICATION NUMBER: 60/080328
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PRIOR FILING DATE: 1998-04-15
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PRIOR APPLICATION NUMBER: 60/081819
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FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082569
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APPLICATION NUMBER: 60/082704
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PRIOR FILING DATE: 1998-03-27
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PRIOR FILING
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172 CCGTGCGCCAGC-----CTGTGCTGCGGGCACGGCACGTGCATC-----GACGGC 216
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468 ValLys------AspCysProAsnGlyLeuAspGluArgAsnCysValCysArg 483
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| 553 AspGluGluHisCysAspCysGlyLeuGlnGlyProSerSerArgIleVaiGlyGlyAla 572
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592 IleCysGlyGlyAlaLeulleAlaAspArgTrpVallleThrAlaAlaHisCysPheGln 611
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743 LysGlyLysLysAspAlaCysGlnGlyAspSerGlyGlyProLeuValCysLysAlaLeu 762
                                                                                                                                                                            763 SerGlyArgTrpPheLeuAlaGlyLeuValSerTrpGlyLeuGlyCysGlyArgProAsn 782
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PRIOR APPLICATION NUMBER: 60/06220
PRIOR APPLICATION NUMBER: 60/06220
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/077641
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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APPLICATION NUMBER: 60/077791
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APPLICATION NUMBER: 60/078004
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TITLE OF INVENTION: Acids Encodi
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Wood, William I.
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Stewart, Timothy A.
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Goddard, Audrey
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Kuo, Sophia S.
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Gao, Wei-Qiang
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APPLICATION UNMBER: 60/078886
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PRIOR PILING DATE: 1998-04-28
PRIOR PILING DATE: 1998-04-28
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PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
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Alignment Scores:

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APPLICANT: Tumas, Daniel Applicant: Tumas, Daniel Applicant: Williams, P. Mickey Applicant: Williams, P. Mickey Applicant: Wood, William I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630PlC63 CURRENT APPLICATION NUMBER: US/09/999,832A CURRENT FILIG DATE: 2001-10-24
                                                                                1105 CACGGCACCTGGTTCCTGGTGGGCCTGGTGAGCTGGGGGTGTGGGGCTCCTTCAC 1164
1048 GGGGACCGGCAGGATGCCTGCGAGGCGACAGTGGGGGGCCCATGGTCGCC---TCCTTC 1104
                                                                                                     1165 AACTAGGGGGTTTACACCAAAGTCAGCGGCTACCTCGACTGGATC 1209
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CURRENT FILING DATE: 2001-10-24

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-03

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FILING DATE: 1998-03-11
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FILING DATE: 1998-03-12
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FILING DATE: 1998-03-11
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Shelton, David L.
Stewart, Timothy A.
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Gerritsen, Mary E.
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Kuo, Sophia S.
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Page 18

PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
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1105 CACGGCACCTGGTTCCTGGTGGGCCTGGTGGGGTGAGGGCTGTGGGCTTCTCAC 1164
                1165 AACTACGGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATC 1209
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                                                                                                                                             Sequence 169, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                        Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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FILING DATE: 1998-03-13
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Roy, Margaret Ann
Shelton, David L.
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Williams, P. Mickey
Wood, William I.
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Filvaroff, Ellen
Fong, Sherman
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Hillan, Kenneth J
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Kuo, Sophia S.
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                                                                                                                                                                                                          Baker Kevin P.
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                                                                                                                                 US-09-978-189-169
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PRIOR APPLICATION NUMBER: 60/09923
PRIOR APPLICATION NUMBER: 60/09923
PRIOR PILING DATE: 1998-03-30
PRIOR PELICATION NUMBER: 60/080105
PRIOR PELING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
PRIOR PELICATION NUMBER: 60/080105
PRIOR PELICATION NUMBER: 60/080194
PRIOR PELING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080134
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR PELING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-08
PRIOR PELING DATE: 1998-04-09
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DR FILING DATE: 1998-04-01

DR FILING DATE: 1998-04-01

DR FILING DATE: 1998-04-01

DR APPLICATION NUMBER: 60/080333

DR FILING DATE: 1998-04-01

DR FILING DATE: 1998-04-01

DR FILING DATE: 1998-04-01

DR FILING DATE: 1998-04-08

DR APPLICATION NUMBER: 60/081049

DR FILING DATE: 1998-04-08

DR APPLICATION NUMBER: 60/08105

DR PILING DATE: 1998-04-08

DR PILING DATE: 1998-04-09

DR PILING DATE: 1998-04-15

DR PILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
FILING DATE: 1998-04-22
FILING DATE: 1998-04-23
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081952
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FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082569
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APPLICATION NUMBER: 60/082704
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082804
FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/081838
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
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FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
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APPLICATION NUMBER: 60/079663
                     APPLICATION NUMBER: 60/078939 FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/079689
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PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/084639
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084609
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-5-07
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR PILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085329
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085582
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085589
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085589
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
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PRIOR APPLICATION NUMBER: 60/08559
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559 PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-29
PRIOR PLING DATE: 1998-04-29
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R FILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/083554

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R APPLICATION NUMBER: 60/08358 PRIOR APPLICATION NUMBER: 60/085697 APPLICATION NUMBER: 60/083500 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083742 APPLICATION NUMBER: 60/084414 FILING DATE: 1998-05-06 APPLICATION NUMBER: 60/08441 FILING DATE: 1998-05-06 APPLICATION NUMBER: 60/084637 FILING DATE: 1998-04-30 APPLICATION NUMBER: 60/084366 APPLICATION NUMBER: 60/083559 FILING DATE: 1998-04-29 FILING DATE: 1998-05-05 FILING DATE: 1998-05-07 FILING DATE: 1998-04-27 PRIOR PRIOR

Alignment Scores: 2.07e-20 Length: Pred. No.: 470.00 Matches: Score: 46.93% Conservative: Best Local Similarity: 33.07% Mismatches: Query Match: 9

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                                   172 CCGTGCGCCAGC-----CTGTGCTGCGGCACGGCACGTGCATC-----GACGGC 216
                                                                   448 ProCysProGlyGluPheLeuCysSerValAsnGlyLeuCysValProAlaCysAspGly 467
                                                                                                      217 ATCGGCAGCTTCAGCTGCGACTGCCGCAGCGGCTGGGAGGGCCGCTTCTGCCAGCGCGAG 276
                                                                                                                            277 GIGAGCIICCICAAIIGCICGCIGGACAACGGCGGCIGCACGCAIIACIGCCIAGAGGAG 336
                                                                                                                                                                                                           484 AlaThrPhe---GlnCysLysGluAspSer-----ThrCyslleSerLeuProLys 499
                                                                                                                                                                                                                                              337 GTGGGCTGGCGCGCTGTAGCTGTGCGCCTGGCTACAAGCTGGGGGACGACCTCCTGCAG 396
                                                                                                                                                                                                                                                                              397 IGICACCCGCAGIGAAGIICCCIIGIGGGAGGCCCIGGAAGCGGAIGGAGAAGAAGGCGC 456
                                                                                                                                                                                                                                                                                                                                             516 CysGlnGluGlyVal-----ProCysGlyThrPheThrPheGlnCysGlu---Asparg 532
                                                                                                                                                                                                                                                                                                                                                                                      457 AGICACCIGAAA-----CGAGACACAGAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                      533 SercysVallysLysProAsnProGlnCysAspGlyArgProAspCysArgAspGlySer 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GACCAAGTAGATCCGCGGCTCATTGATGGGAAG 522
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| 553 AspGluGluHisCysAspCysGlyLeuGlnGlyProSerSerArgIleValGlyGlyAla 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              523 ATGACCAGGCGGGGAGACAGCCCCTGGCAGGTGGTCCTGCTGGACTCAAAGAAGAAGCTG 582
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688 GluProGlyLeuHisCysTrpIleThrGlyTrpGly-----AlaLeuArgGluGlyGly 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   868 CAGGCCGGCCAGGAGACCCTCGTGACGGCTGGGGCTACCACAGCAGCGGGAGAGGAG 927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       706 ProlleSerAsn-----AlaLeuGlnLysValAspValGlnLeulleProGlnAsp 722
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US-09-763-153-1 (1-1245) x US-09-978-189-169 (1-802)
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763 SerGlyArgTrpPheLeuAlaGlyLeuValSerTrpGlyLeuGlyCysGlyArgProAsn 782
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                                 1165 AACTACGGCGTTTACACCAAAGTCAGCCGCTACCTCGACTGGATC 1209
                                                        783 TyrPheGlyValTyrThrArglleThrGlyVallleSerTrplle 797
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CURRENT FILING DATE: 2001-10-16.
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
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Mismatches:
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Matches:
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Goddard, Audrey
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Filvaroff, Ellen
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Kuo, Sophia S.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Publication No. US20C
GENERAL INFORMATION:
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Best Local Similarity:
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US-09-978-608A-169
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LENGIH: 802
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                                                                          397 TGTCACCCCCAGTGAAGTTCCCTTGTGGGAGGCCCTGGAAGCGGATGGAGAAGAAGCGC 456
                                                                                                               516 CysGlnGluGlyVal----ProCysGlyThrPheThrPheGlnCysGlu---AspArg 532
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337 GIGGGCIGGCGGCGCTGIAGCIGIGCGCCTGGCIACAAGCIGGGGACGACCTCCTGCAG 396
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Patent No. US20020064856A1
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APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: GRENEFEEL, SEAN
APPLICANT: CHARIDCZAK, GLEN
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APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
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988 GAGTGCAGCGAGGTCATGAGCAACATGGTGTCTGAGAACATGCTGTGTGCGGGCATCCTC 1047
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                                                                 CAGGCCGGCCAGGAGCCCTCGTGACGGGCTGGGGCTACCACAGCAGCCGAGAGGAG
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TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT PELLING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
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Patent No. US20020064856A1
GENERAL INFORMATION:
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CHARYDCZAK, GLEN
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APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 108
LENGTH: 850
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Best Local Similarity:
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955 AACTTCATCAAGATTCCCGGTGGTCCCGCACAATGAGTGCAGCGAGGTCATGAGCAACATG 1014
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523 LeuPheCysValSerProGlnProAlaCysAsnThrSerSerPheArgGlnHisGlyPro 542
                                   ----CTGGACAACGCGGCTGCACGCATTACTGCCTAGAG 333
                                                                 LeuIleCysAspGlyPheArgAspCysGluAsnGlyArgAspGluGlnAsnCysThrGln 562
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668 AlaHisLeuClyMetTyr---ValGlnGlyAsnAlaLysPheVal-----SerProVal 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 721 AAGGAGGICTICGTCCACCCCAACTACAGCAAGAACACCACCGACAATGACATCGCACTG 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     741 GlyTrpGly------ArgArgHisGluAlaAspAsnLysGlySerLeuValLeu 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        757 GlnGlnAlaGluValGluLeuIleAspGlnThrLeuCysValSerThrTyr---GlyIle 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                496 GTAGATCCGCGGCTCATTGATGGGAAGATGACCAGGCGGGGAGACAGCCCCTGGCAGGTG
                                                                                                                                                                                                                                                                                                                          556 GICCIGCTGGACTCAAAGAAGAGCTGGCCTGCGGGGCAGTGCTCATCCACCCCTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                        628 ValSerLeuHisPheValGlySerAlaTyrCysGlyAlaSerVallleSerArgGluTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        616 GTGCTGACAGCGCCCACTGC------ATGGATGAGTCCAAGAAGCTCCTT
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725 ProProThrGlyGlnArgValArg------SerGlyGluLysCysTrpValThr
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                                                                                                                                                                                                   579 PheArgLysGlnAsnAlaLysCysAspGlyThrValAspCysProAspGly-----
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Search completed: March 17, 2003, 19:04:48

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